

FIGURE 1

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTGCTGTTTCTT
CTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAAGAGGAAGGGGCAAGGGCG
GCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACCTGGTGTACGGATGAAACCGTATGCCC
GCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAG
AGAAAGTGTGAGGTCAACTTGCAGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCAT
CAACCACGACCCAGCCGTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACC
CCTTCACCATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCCCTGTGCGCCGCCGC
CTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCTG
CACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGACCATCCTCCTTGACCTTT
GTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

FIGURE 2

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYERNIEEMVA
QLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGCVNPFTMQEDRSMVSV
VFSQVPVRRRLCPPPRTGPCRQRAVMETI AVGCTCIF

FIGURE 3

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCC
TGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCACAGTCAC
GGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGG
TGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGC
ACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC
CAGCGCTCCATCTCACCCCTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTT
CGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGC
GGCTGCTCCAGAGCCTGCTGGTGTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT
GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGCGCTGCACCTGCGTGCTGCCCCGTTTCACT
GTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCTATTTATGTG
TATTTATTGTTATTTATATGCCTCCCCAACACTACCCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGAC
AGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGC
CCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCTGCTCCCGGCTTCCCT
TACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTA
ACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

FIGURE 4

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLE
AASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKLAFAECLCRGCIDARTGRE
TAALNSVRLQLSLLVLRRLRRRPCRDRGSGGLPTPGAFHTEFIHVPVGCTCVLPRSV

| | |
|---------------------------------------|------------------------------------|
| Signal peptide: | Amino acids 1-18 |
| Tyrosine kinase phosphorylation site: | Amino acids 112-121 |
| N-myristoylation sites: | Amino acids 32-38;55-61;133-139 |
| Leucine zipper pattern: | Amino acids 3-25 |
| Homologous region to IL-17: | Amino acids 99-195 |

FIGURE 5

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGTCAGTCA
GTGCCCCGACTTGTGACTGAGTGTGCAGTGCCAGCATGTACCAGGTCAGTGCAGAGGGCTGCCTGAGGGCT
GTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGCTGCCAGGTTTGGGGCTGG
GGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGATGAGGGAGCGACCCAGATTAGGTGA
GGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCATTCTTGGCAATGGTCATGGGAACCCACACCT
ACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT
GTGCCTGTGCCTCCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGA
CCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGA
CCTGTACCACGCCCCGTTGCCTGTGCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGG
GCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACC
CACAAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGTGT
GATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACAACCACTTG
CCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCGTGAAGTGCTGTCTGGAGCAGCAGGATCCCCGGGAC
AGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAGCAGCTGCTGCTTAGGGCCGC
CGGAAGCTGGTGTCTGTCATTTTCTCTCAGGAAAGGTTTTCAAAGTTCTGCCCATTTCTGGAGGCCACCA
CTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTGGCCCAGCACAGGCACTTCTAGATATTTCCCC
CTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATTTGTTTGTGTTTACTCATCACTCAGTGAGCATCTACTTTGG
GTGCATTCTAGTGTAGTTACTAGTCTTTTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATA
GAGATTTATCCAAATAAATATCTTTATTTAAAAATGAAAA

FIGURE 6

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPKQDTSEELLRWSTVPVPPLEPARPNRHP
ESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSELLYHNQTVFYR
RPCHGEKGTGTHKGYCLERRLYRVSLACVCVRPRVMG

| | |
|---------------------------------------|---------------------------|
| Signal peptide: | Amino acids 1-32 |
| N-glycosylation site: | Amino acids 136-140 |
| Tyrosine kinase phosphorylation site: | Amino acids 127-135 |
| N-myristoylation sites: | Amino acids 44-50;150-156 |

FIGURE 7

ATGCTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCAGGGCGGGCAGGCG
CCCCGCGCGGCCGCGGGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGG
CCGGCGTGCTCAGTGCCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCGAGCTGC
CCGGCAGGGGGCAGGCCCCGGCGACCGCCGCTTCCGGCCGCCACCAACCTGCGCAGCGTGTGCCCTGGGC
CTACAGAATCTCCTACGACCCGGCGAGGTACCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCT
GCCTGACCGGGCTGTTCCGGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCGTGTCTACATGCCACCGTCGTC
CTGCGCCGCACCCCCGCCTGCGCCGGCGGGCCGTTCGTCTACACCGAGGCCTACGTCACCATCCCCGTGGG
CTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCCA
AGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCCTGAGGCCGGTCTGCCCCGGGAGGTCTCCCCGG
CCCGCATCCCGAGGCGCCCAAGCTGGAGCCGCGCTGGAGGGCTCGGTCCGGCGACCTCTGAAGAGAGTGCACC
GAGCAAACCAAGTGCCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGG
GCATCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACCCGGCACGG
GCATCCTGTGTGCGGCCCGCATGGAGGGTTTGAAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATC
GGCTGCTGCGGGTGCAGGGCGTGA CTACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTTTT
AAAGCAATCTAAAAATAATAATAAGTATAGCGACTATATACCTACTTTTAAATCAACTGTTTTGAATAGA
GGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTT
ACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTTGTAGCTGGTACACTCTGG
CCTGGGTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGTCTCATCTGACCCACTC
TTCCTTCCACTGAAGGTCTTCACGGGCCCTCCAGGTGGACCAAAGGGATGCACAGGCGGCTCGCATGCCCCA
GGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACCTCGC
ACAATTTTTTCCCCCTTTTGAAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGA
ACGTGACATCTTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCA
GGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCTGTTTCTGCA
TTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGTCTCTGAACACAATTATTTGT
AAAAGTTAGTAGTTCTTTTTTAAATCATTAAAAGAGGCTTGCTGAAGGAT

FIGURE 8

MLVAGFLLALPPSWAAGAPRAGRPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASC
PAGGRPGDRRFRPPTNLRVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGCEEDVRFRSAPVYMPTVV
LRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQAKLLLGPNDAPAGP

| | |
|---------------------------------------|---|
| Signal peptide: | Amino acids 1-15 |
| N-glycosylation sites: | Amino acids 68-72;181-185 |
| Tyrosine kinase phosphorylation site: | Amino acids 97-106 |
| N-myristoylation sites: | Amino acids 17-23;49-55;74-80; 118-124 |
| Amidation site: | Amino acids 21-25 |

FIGURE 9

CAACTGCACCTCGGTTCTATCGATAGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCAT
GGTCAAGTACTTGCTGCTGTCGATATTGGGGCTTGCCCTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCA
AAGTAGGACATACTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGAC
ATTGGCATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGAACTTGG
GCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAAGAGACCCTGGTCGTC
CGGAGGAAGCACCAAGGCTGCTCTGTTTCTTCCAGTTGGAGAAGGTGCTGGTGAAGTGTGGCTGCACCTG
CGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCCACTCAGCTGAAGAAG

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FIGURE 10

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINENQRVSMS
RNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSVSFQ
LEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

Amino acids 1-30

N-glycosylation site:

Amino acids 83-86

N-myristoylation sites:

Amino acids 106-111;136-141

FIGURE 11

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGT
TCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGACTTGA
GGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCAATTTTGATGAATGTAAGC
TGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAA
CTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGGCCCTTCCAGACTCAGACCAGACCCTCTGGTG
GTAAATGGACATTTTCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAAT
ATTCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTTCACCTCACCAGGCTGCCTAGA
CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTA
AGAAGAATGAGGAGACAGTAGAAGTGAACCTTCAACCACTCCCCTGGGAAACAGATACATGGCTCTTATC
CAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGT
GGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGACAGCTGACTCCATATTTTCTACTTGTGGCA
GCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCCAAACAGGCGTCCCTTTCCCTCTGGATAAC
AACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT
GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGC
CCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAA
TTTCTTCAAAACCATTGCAGAAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGG
TCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCA
ACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCC
CTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCTACTT
TAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATG
CCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAGCCTGC
CACGATGGCTGCTGCTCCTTGTAG

FIGURE 12

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRVEPVTTTSVATGDYSILMNVS
WVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPTVGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKQQVSAGKRSQACHD
GCCSL

Signal sequence:

Amino acids 1-14

Transmembrane domain:

Amino acids 290-309

N-glycosylation sites:

Amino acids 67-70;103-106;156-159;
183-186;197-200;283-286

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 228-231;319-322

N-myristoylation site:

Amino acids 116-121

Amidation site:

Amino acids 488-491

FIGURE 13

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGGACAGAG
AGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATTCCAGCCCCCTGCCA
CCCACAGACACGGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGGAGCACAGGGCCTCAGGCCTGGGT
GCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGCTGTCTTGGCACTGGGCGGAAGCCCAGTGG
TCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTC
TGGGACAGTGACATACTCTGCCTGCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCA
CCTGCAGACAGAGCTGGTGTCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCC
ACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGG
GTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTACTGCCCG
CTGCGTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATAT
GACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCCCTATACTCAGCCCAGGTACGAGAAGGA
ACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTCTCAGCAGATGGTGACAACGTGCATC
TGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCA
AAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTG
CCTCTGTATTACAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCCTCAGGGAGGACC
CCCGCGCACACCAGAACCTCTGGCAAGCCGCCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCTGGAC
GCACCGTGTCTGCTGCCCCGAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACT
GGTCCCACCGCTTTCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACC
CTAACCTCTGTGTTTCAAGTGAACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTG
GGGCCTCTCAAAGACGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTT
GGAACCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTAC
TACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCC
ATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTC
CCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCGCTCGG
GGGCGGCCCGCAGGGGCCGCGCGGCTCTGCTCCTTACTCAGCCGATGACTCGGGTTTCGAGCGCCTGGTG
GGCGCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGACCTGTGGAGCCGTCGTGAAC
GAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAGCGGCCAGACCCTGCAGGAGGGCGGCGTGGTGG
TCTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCCGGG
GCGCACGGCCCCGACGACGCCTTCCGCGCCTCGCTCAGCTGCGTGTGCCCCACTTCTTGACAGGGCCGGG
GCCCCGACGTACGTGGGGGCTGCTTCGACAGGCTGCTCCACCCGACGCCGTACCCGCCCTTTTCCGCA
CCGTGCCCCGTCTTCACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCG
CGTTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCCAGCCAGCCCTGGATAGCTACTT
CCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGACGGGA
CTTAAATAAAGGCAGACGCTGTTTTCTAAAAAA

FIGURE 14

MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGPVLAPTHLQTELV
 LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVLSFQAYPTARCVLLEV
 QVPAALVQFGQSVGSSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSAADGNVHLVNLVS
 EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN
 LWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
 VNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
 GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSAAAARG
 RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFHAQRRQTLQEGGVVLLFSP
 GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT
 LPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

signal sequence:

Amino acids 1-20

transmembrane domain:

Amino acids 453-473

N-glycosylation sites:

Amino acids 118-121;186-189;198-201;
 211-214;238-241;248-251;334-337;
 357-360;391-394

Glycosaminoglycan attachment site: Amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-555

N-myristoylation sites:

Amino acids 107-112;152-157;319-324;
 438-443;516-521;612-617;692-697;
 696-701;700-705

FIGURE 15

CGAGGGCTCCTGCTGGTACTGTGTTCTGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAGGCCATGCAG
CCATGTTCCGGGAGCCCTAATTGCACAGAAGCCCCATGGGGAGCTCCAGACTGGCAGCCCTGCTCCTGCCTC
TCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGCTTTCGCCACCTGCCCCACTGGAACACC
CGCTGTCTCTGGCCTCCACACGGATGACAGTTTCACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTG
GTGGGCCCTCTTCTCCACAAAGCCTTGGTGTGTGCGAGTCTGGCACTGTTCCCGCTGTTTGTGCCAGCATCTGC
TGTCAGGTGGCTCAGGTCTTCAACGGGGCCTCTTCCACCTCCTGGTGCAGAAATCCAAAAGTCTTCCACA
TTCAAGTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTCACCTGTCT
TGAGAAGAGCCATCACATTTCCATCCCCCTCCCAGACATCTCCACAAGGGACTTCGCTCTAAAAGGACCC
AACCTTCGGATCCAGAGACATGGGAAAGTCTTCCAGATTGGACTCACAAAGGCATGGAGGACCCGAGTTC
TCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTCCGGGTGACCATATCTTCAGGCCCTGAGGTGAGCGTGCG
TCTTTGTCAACAGTGGGCACTGGAGTGTGAAGAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTG
GGGGCCACACTGTAGAGCTGCCTTATGAATTCCTTCTGCCCTGTCTGTGCATAGAGGCATCTACCTGCAA
GAGGACACTGTGAGGCGCAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAA
GTCAGTGCACCTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCCCACTGA
AGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATACCTTTTGCAAAGACCTCCCGAATGCCACGGCT
CGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCCCAGCTCTGCTTCAAGTTCTCTTT
TGGAACAGCAGCCATGTTGAATGCCCCCACCAGACTGGGTCTCTCACATCCTGGAATGTAAGCATGGATA
CCCAAGCCCAGCAGCTGATTCTTCACTTCTCCTCAAGAATGCATGCCACCTTCACTGCTGCCTGGAGCCTC
CCAGGCTTGGGGCAGGACACTTTGGTGCCCCCGTGTACACTGTGAGCCAGGCCCGGGGCTCAAGCCCAGT
GTCACTAGACCTCATCATTTCCCTTCCCTGAGGCCAGGGTGCTGTGTCTGCTGGTGTGGCGGTGAGATGTCCAGT
TTGCCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCACTGCTG
GCCCTCCTCACCTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCACAGTCAGGCCCGGGCCAGC
GCGGCCAGTGCTCCTCCTGCACGCGGCGGACTCGGAGGCGCAGCGGCGCCTGGTGGGAGCGCTGGCTGAAC
TGCTACGGGCAGCGCTGGGCGGCGGGCGGACGTGATCGTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGT
GGGGCCGCTGCCGTGGCTCTGGGCGGCGGCGGACGCGGTAGCGCGGAGCAGGGCACTGTGCTGCTGCTGT
GGAGCGGCGCCGACCTTCGCCCCGTGAGCGGCCCCGACCCCCGCGCGCCCCCTGCTCGCCCTGCTCCAC
GCTGCCCCGCGCCCGCTGCTGCTGCTCGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCGCC
GCTGCGCGCCCTGCCGCGCTACCGCCTGCTGCGCGACCTGCCGCGTCTGCTGCGGGCGCTGGACGCGCGGC
CTTTGCGAGAGGCCACCAGCTGGGGCCGCTTGGGGCGCGGCGAGCGCAGGCAGAGCCGCTAGAGCTGTGC
AGCCGGCTTGAACGAGAGGCCCGCCGACTTGACAGACCTAGGTTGAGCAGAGCTCCACCGCAGTCCCCGGTGTCT

FIGURE 16

MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSFSGSSAYIPCRTWWALFSTKPWCV
RVWHCSRCLCQHLLSGGSLQRGLFHLLVQKSKKSSTFKFYRRHKMPAPAQRKLLPRRHLSEKSHHISIPS
PDISHKGLRSKRTQPSDPETWESLPRLDSQRHGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHQWALECE
ELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQH
TQMVMALTLRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKFSFGNSSHVECPH
QTGSLTSWNVSMQTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDLIIPFLR
PGCCVLVWRSDVQFAWKHLLCPDVSYRHLGLLILALLALLTLLGVVLALTCTRRPQSGPGPARPVLLHAAD
SEAQRRLVGALAEELLRAALGGGRDVIIVDLWEGRHVARVGPLPWLWAARTRVAREQGTVLLLWSGADLRPVS
GPDPRAPLLALLHAAPRPLLLLAYFSRLCAKGDIPPLRALPRYRLRLRDLPRLLRALDARPF AEATSWGR
LGARQRRQSRLELC SRLEREAA RLADLG

| | |
|--|-------------------------------------|
| Signal peptide: | Amino acids 1-23 |
| Transmembrane domain: | Amino acids 455-472 |
| N-glycosylation sites: | Amino acids 318-322;347-351;364-368 |
| Glycosaminoglycan attachment site: | Amino acids 482-486 |
| cAMP- and cGMP-dependent protein kinase phosphorylation sites: | Amino acids 104-108;645-649 |
| Tyrosine kinase phosphorylation site: | Amino acids 322-329 |
| N-myristoylation sites: | Amino acids 90-96;358-364;470-476 |
| Eukaryotic cobalamin-binding proteins: | Amino acids 453-462 |

FIGURE 17

GCCAGGCCCTATCTCCCTGCCAGGAGGCCGAGTGGGGGAGGTGAGACGGGGCGGTTGGAGGGGGAGGGAT
GCCACGCGCTTCTGCCTCAGGTGTTCTCGCTTGTTTGTTCAGTGGAGAGCAGGGAGTGGGGCCAGCCAGCA
GAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAG
CATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAT
TCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGT
CGGAGGGAAGACAGTGCCAACAACCTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAGAACT
GGAATGGAATCTCAACCTTTCTGAATATGAAATTTGAAACGGATTATTTTCGTAAAGGTTGTCCCTTTTCC
TTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGC
CGGACAATCTAGCTTGTAACCCCTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGC
AGGTGTCTCTCGACCACGCACCGCATGGCTCGGACATGCAGGTGTCTTCGACCACGCACCGCACAACTTC
GGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAGCA
GGAGCAAACCTACAGAGATGACCAGCTGCCTCCTTCAAATGTTTCTCCAGGGGATTATATAATTGAGCTGG
TGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCCTCCCGTGGGCGGG
CCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGAT
GTGCCGCAAGAAGCAACAAGAAAATATATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACA
CTGCAGCACTCCCAAGAGAGAGGCTCCGGCCGCGGCCGAAGGTCTTCTCTGCTATTCCAGTAAAGATGGC
CAGAATCACATGAATGTCGTCCAGTGTTTTCGCCTACTTCCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCT
GGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAGAATGGGTCTCCAGAAGATCCACGAGT
CCCAGTTCATCATTGTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAA
GGAGGTGGCCGAGGCTCGGGGAAAGGAGAGCTCTTCTGGTGGCGGTGTGAGCCATTGCCGAAAAGCTCCG
CCAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCTTGCGAGG
GAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTTCC
CACCTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGGCAGCAGAAGGAACCTA
CTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGC
CCGACTGGTTCGAAAAGCAGTTCGTTCCCTTCCATCCTCCTCCACTGCGCTACCGGGAGCCAGTCTTGAG
AAATTTGATTTCGGGCTTGTTTTAAATGATGTGATGTGCAAAACCAGGGCCTGAGAGTGACTTCTGCCTAAA
GGTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCAGCACGAGAGTCAGCATGGGGGCCTGG
ACCAAGACGGGGAGGCCCGCCTGCCCTTGACGGTAGCGCCGCCCTGCAACCCCTGCTGCACACGGTGAAA
GCCGGCAGCCCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTC
TCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGAAACGTCTTCCCTGACGGAGAGCGTGTCTCCT
CTTCAGGCCTGGGTGAGGAGGAACCTCCTGCCCTTCTTCCAAGCTCCTCTCTTCTGGGTGATGCAAAGCA
GATCTTGGTTGCCGAGCTACACTGATGAACTCCACGCGGTGCCCCCTTTGTAACAAAACGAAAGAGTCTA
AGCATTGCCACTTTAAAAA

FIGURE 18

MPRASASGVPA LFVSGEQGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVT
 ILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF
 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHGSDMQVSFDHAPHN
 FGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA
 GPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKD
 GQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKH
 KGGGRGSGKGELFLVAVSAIAEKLQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLS TKYRLMDNLPQLC
 SHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEDWFEKQFVFPFHPPLRYREPVL
 EKFD SGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAQLLHTV
 KAGSPSDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPALPSKLLSSGSK
 ADLGCRSYTDELHAVAPL

Transmembrane domain:

Amino acids 283-307

N-glycosylation sites:

Amino acids 31-34;38-41;56-59;
113-116;147-150;182-185;266-269

Glycosaminoglycan attachment sites: Amino acids 433-436;689-692

cAMP- and cGMP-dependent protein kinase phosphorylation:

Amino acids 232-235

Tyrosine kinase phosphorylation sites: Amino acids 312-319;416-424

N-myristoylation site:

Amino acids 19-24;375-380;428-433;
429-434;432-437;517-522;574-579;
652-657;707-712

h-IL17 1 MTPGKTSLVSL L L L S L E A I V K A G I T I P R
h-IL17B 1 MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGGQRP L A P G P
h-IL17C 1 M T L P G L L F L T W L H T C L A H H D P S L R G H P H S H G T P H C Y S A E E L P L G Q A P P H
h-IL17D 1 M L V A G F L L A L P P S W A A G A P R A G R R P A R P R G C A D R P
h-IL17E 1 M R E R P R L G E D S S L I S L F L Q V V A F L A M V M G T H T Y S H
h-IL17F 1 M T V K T L H G P A M V K Y L L L S I L G L A F L S E A A A R K I P K V G

h-IL17 30 N P G C P N S E D K N F P R T V M V N L N I H N R N T N T N P K R S S D
h-IL17B 43 H Q V P L D L V S R M K P Y A R M E E Y E R N I E E M V A Q L R N S S E L A Q R K C E V N L Q L W M
h-IL17C 51 L L A R G A K W G Q A L P V A L V S S L E A A S H R G R H E R P S A T T Q C P V L R P E E V L E A D
h-IL17D 36 E E L L E Q L Y G R L A A G V L S A F H H T L Q L G P R E Q A R N A S C P A G G R P A O R R F R P P
h-IL17E 36 W P S C C P S K G Q D T S E E L L R W S T V P P P L E P A R P N R H P E S C R A S E D G P
h-IL17F 38 H T F F Q K P E S C P P V P G G S M K L D I G I I N E N Q R V S M S R N

h-IL17 66 Y Y N R S T S P W N L H R N E D P E R Y P S V I W E A K C R H L G C I N A D - G N V D Y H M N S V P
h-IL17B 93 S N K R S L S P W G Y S I N H D P S R I P V D L P E A R C L C L G C C V N P F T M Q E D R S M V S V P
h-IL17C 101 T H Q R S I S P W R Y R V D T D E D R Y P Q K L A F A E C L C R G C I D A R T G R E T A A L N S V R
h-IL17D 86 T N L R S V S P W A Y R I S Y D P A R Y P R Y L P E A Y C L C R G C L T G L F G E E D V R F R S A P
h-IL17E 82 L N S R A I S P W R Y E L D R D L N R L P Q D L Y H A R C L C P H C V S L Q T G S H M D P R G N S E
h-IL17F 74 I E S R S T S P W N Y T V T W D P N R Y P S E V V Q A Q C R N L G C I N A Q - G K E D I S M N S V P

h-IL17 115 I Q E I L V L R R E P P H C P N S F R L E K I L V S V G C T C V T P I V H H V A
h-IL17B 143 V F S Q V P V R R R L C P P P P R T G P C R Q R A V M E T I A V G C T C I F
h-IL17C 151 L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V L P R S V . . .
h-IL17D 136 V Y M P T V V L R R T P A C A G G R S V Y T E A Y V T I P V G C T C V P E P E K D A D
h-IL17E 132 L L Y H N Q T V F Y R R P C H G E K G T H K G Y C L E R R L Y R V S L A C V C V R P R V M G . .
h-IL17F 123 I Q E T L V V R R K H Q G C S V S F Q L E K V L V T V G C T C V T P I V H H V Q

h-IL17D 179 S I N S S I D K Q G A K L L L G P N D A P A G P X

FIG. 19

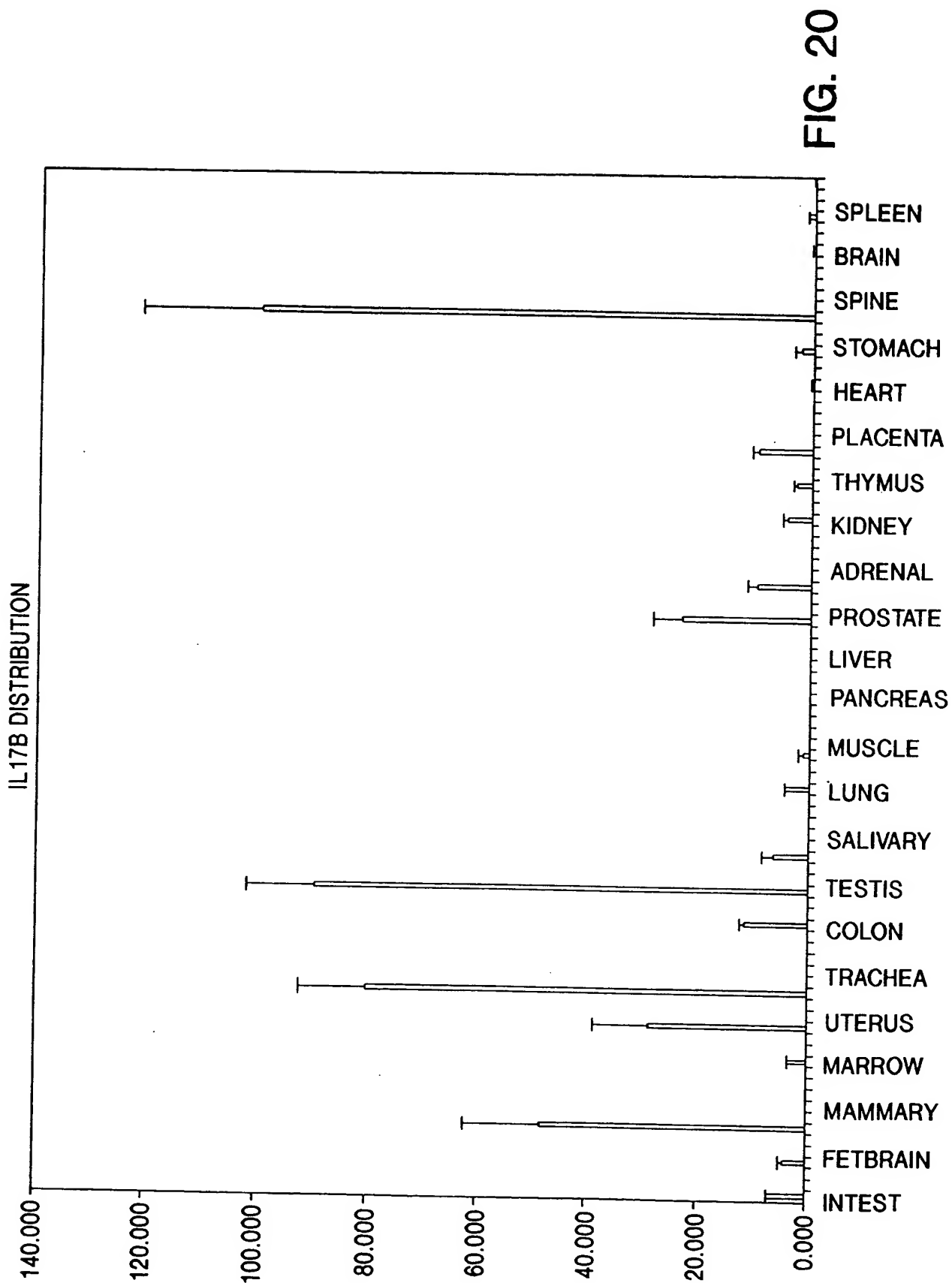


FIG. 20

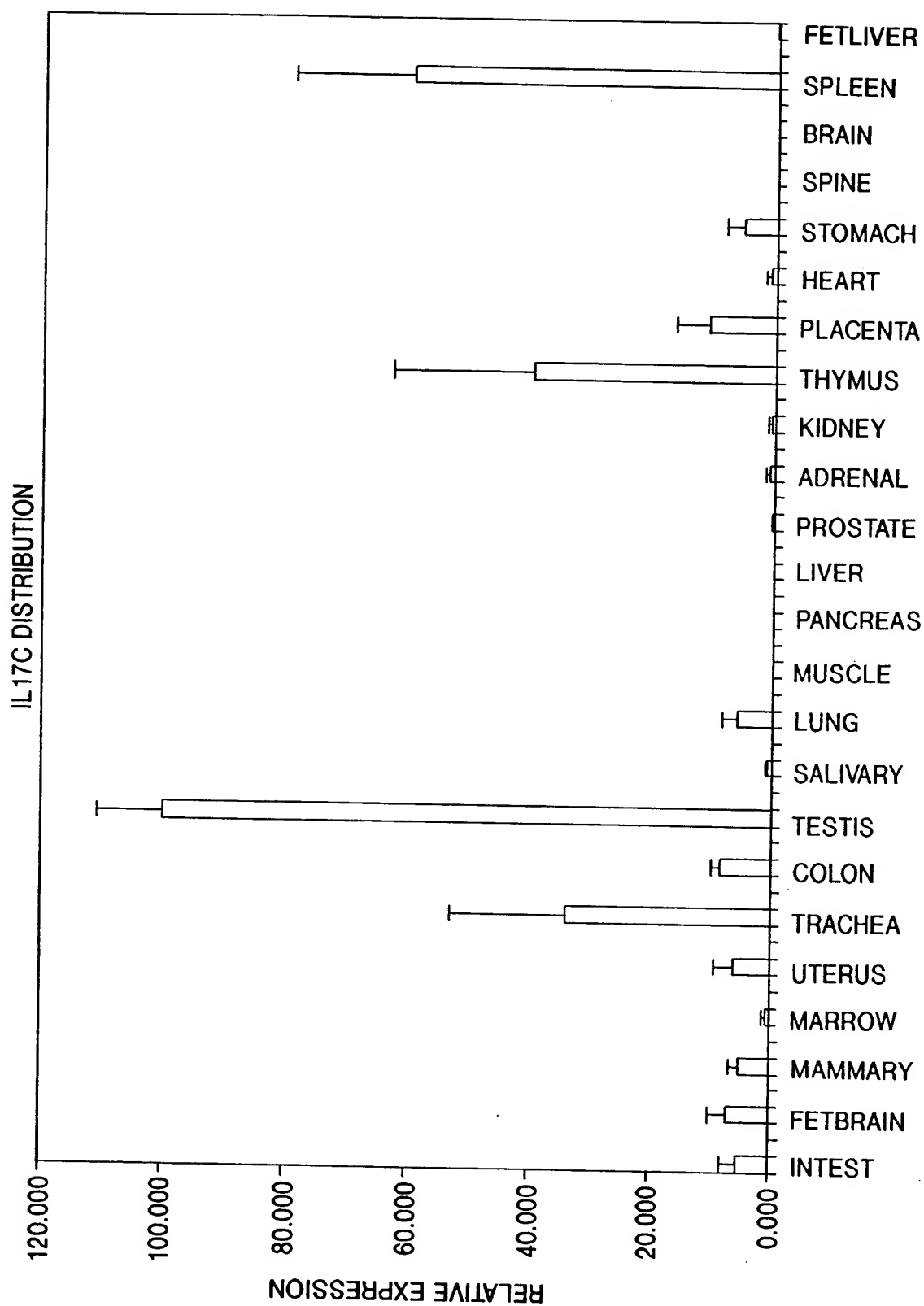
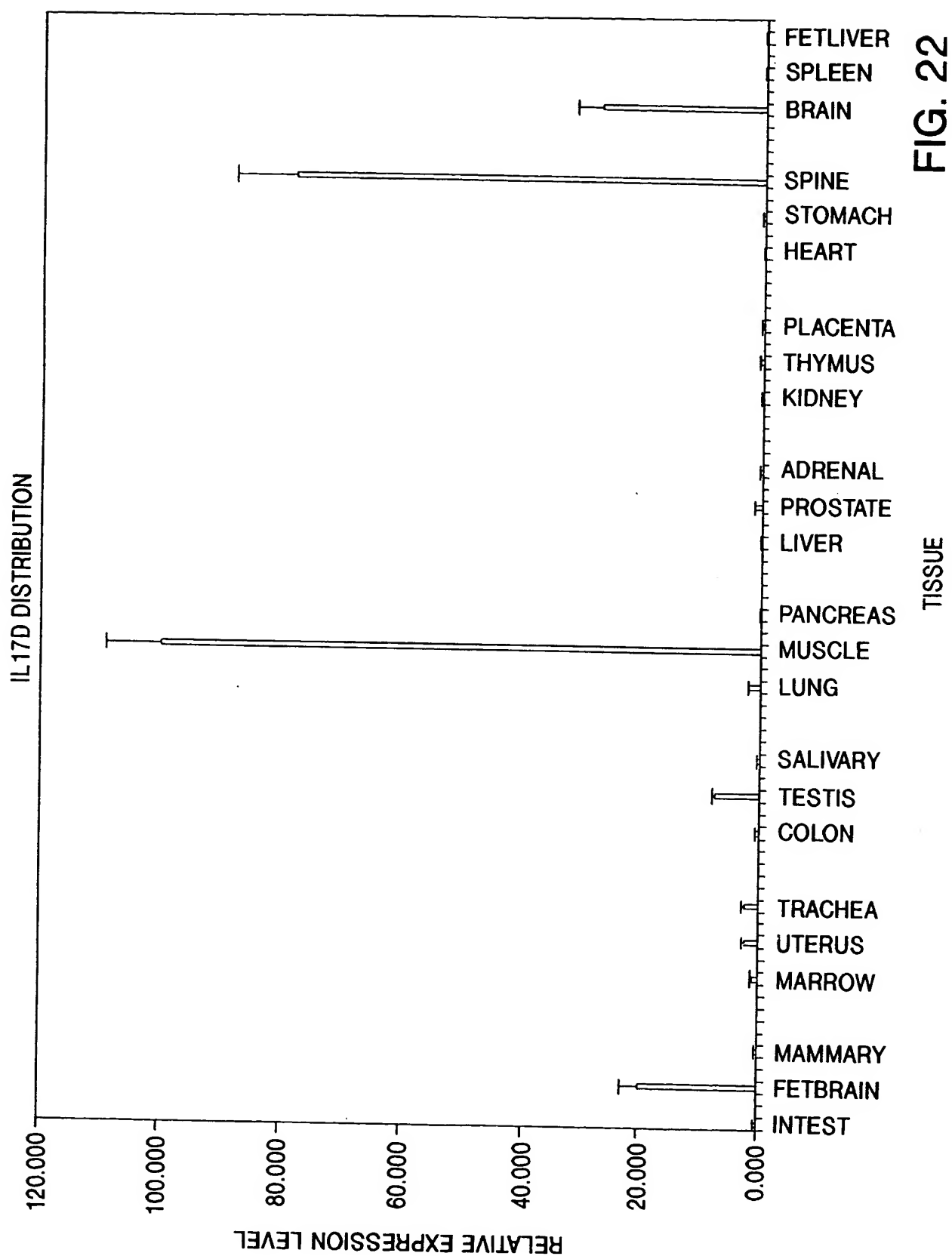
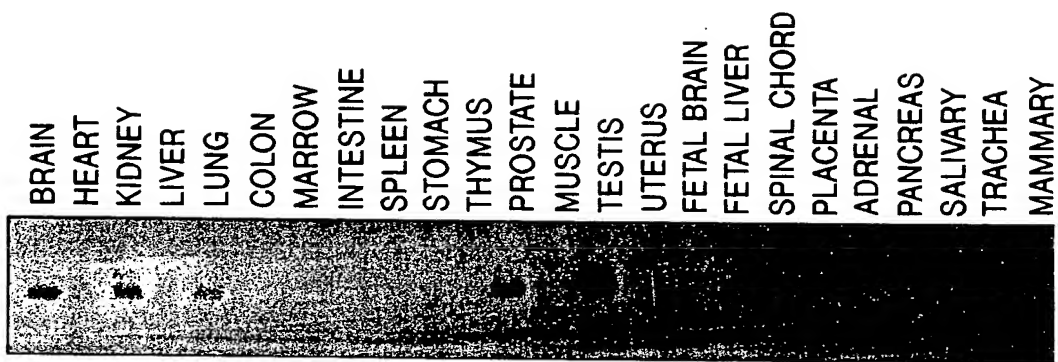


FIG. 21





BRAIN
HEART
KIDNEY
LIVER
LUNG
COLON
MARROW
INTESTINE
SPLEEN
STOMACH
THYMUS
PROSTATE
MUSCLE
TESTIS
UTERUS
FETAL BRAIN
FETAL LIVER
SPINAL CHORD
PLACENTA
ADRENAL
PANCREAS
SALIVARY
TRACHEA
MAMMARY

FIG. 23

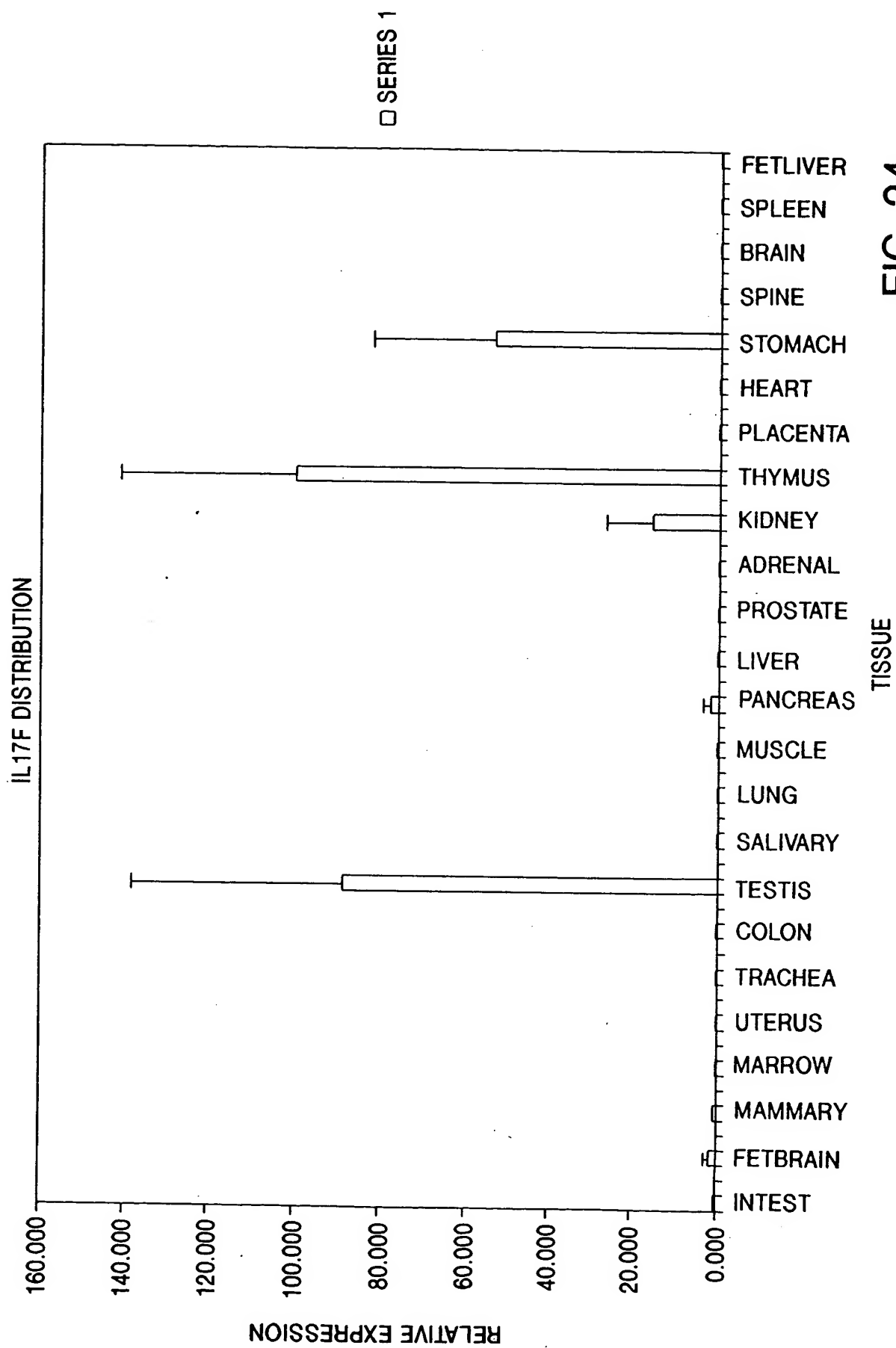


FIG. 24

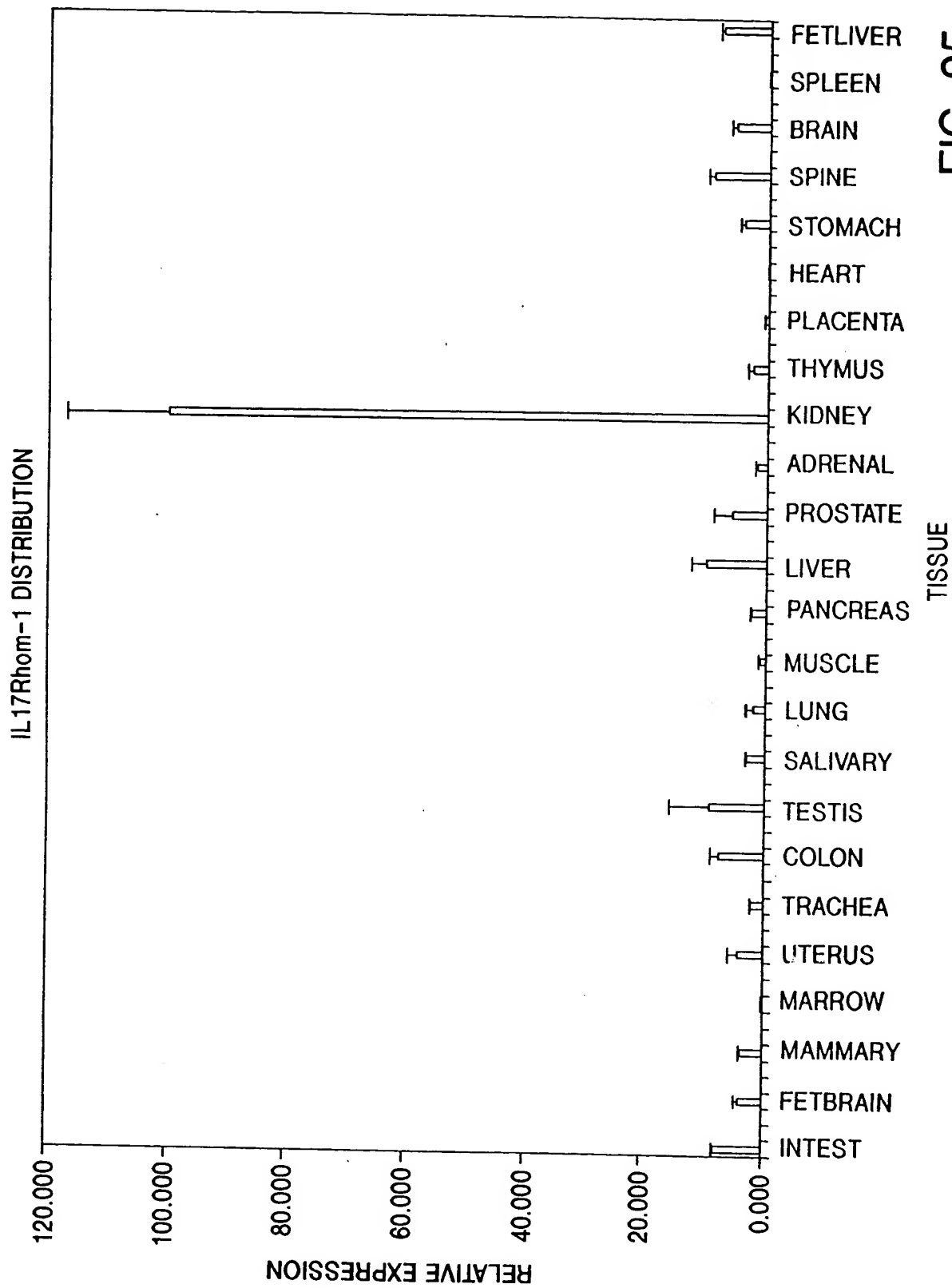


FIG. 25

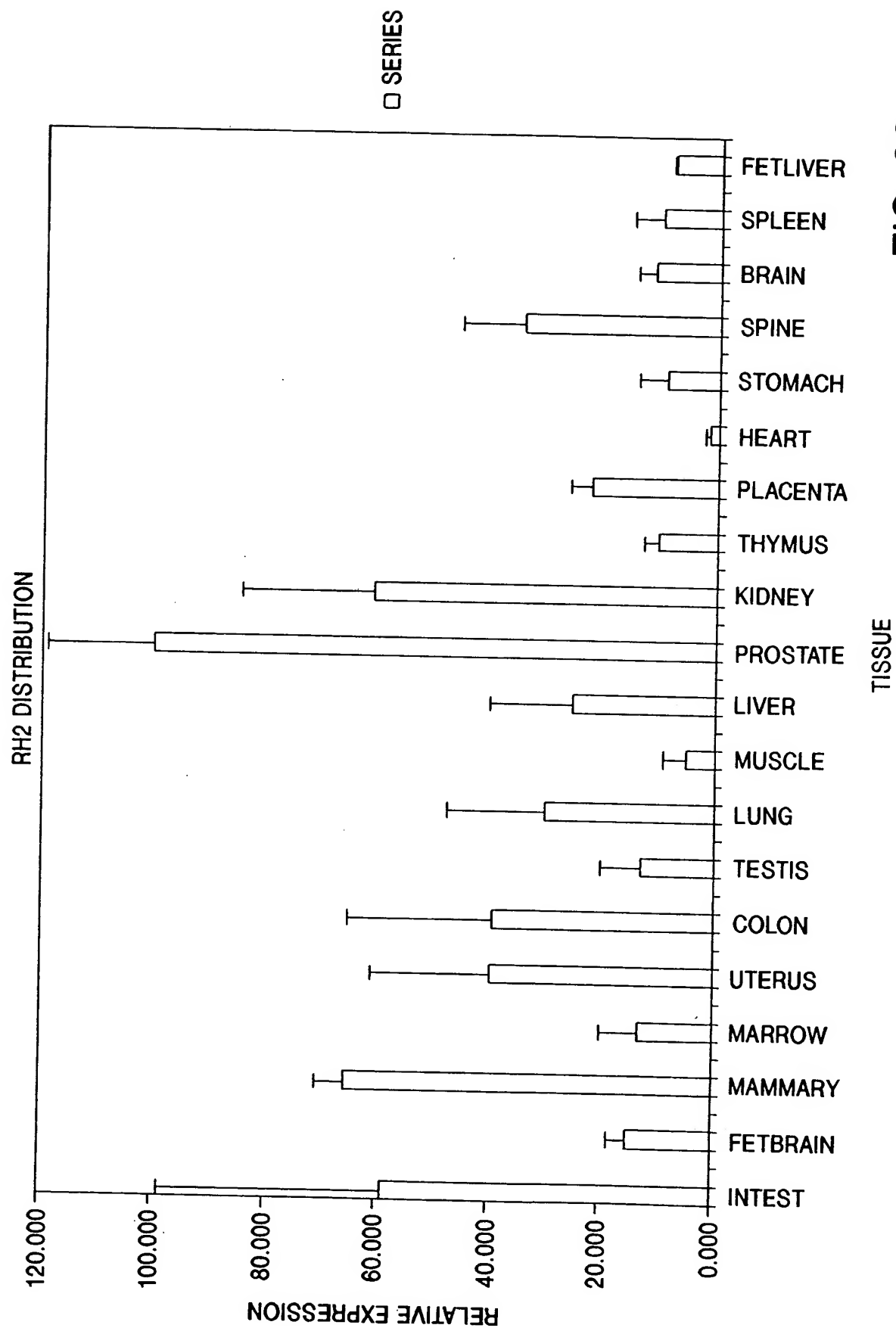


FIG. 26

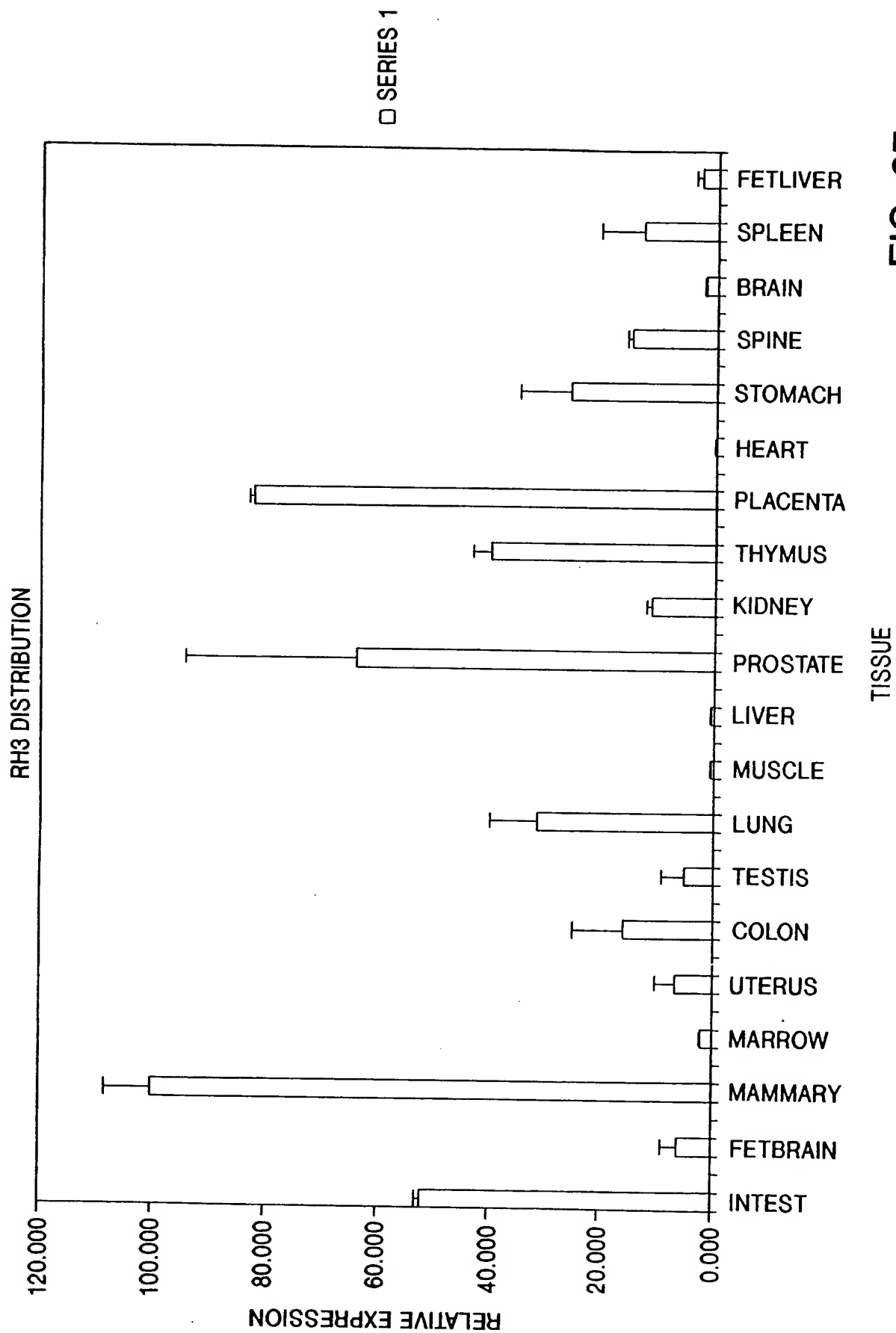


FIG. 27

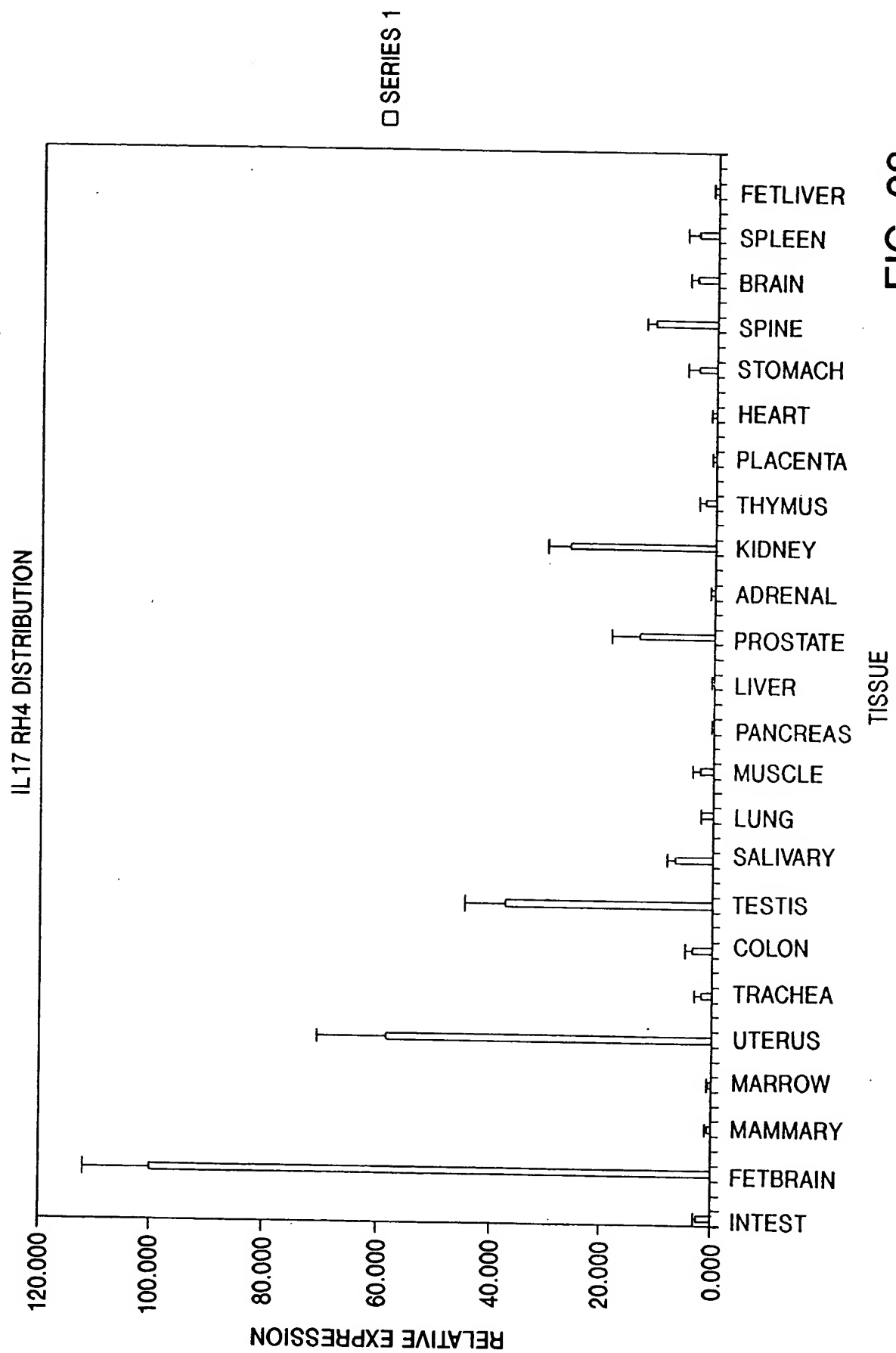


FIG. 28

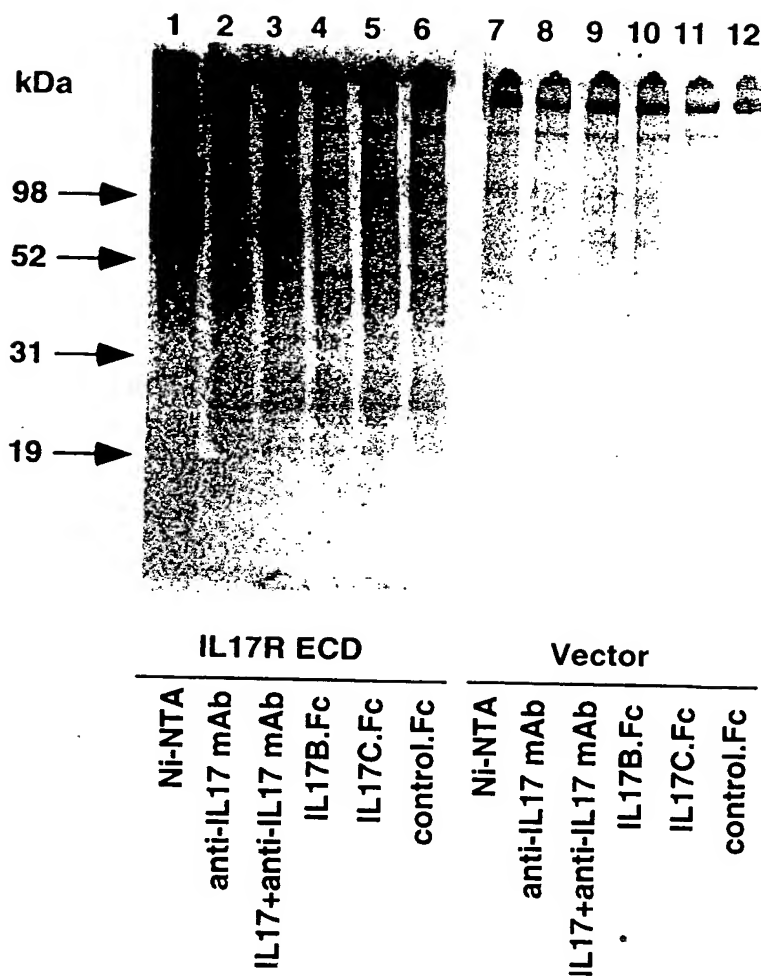


FIG. 29A

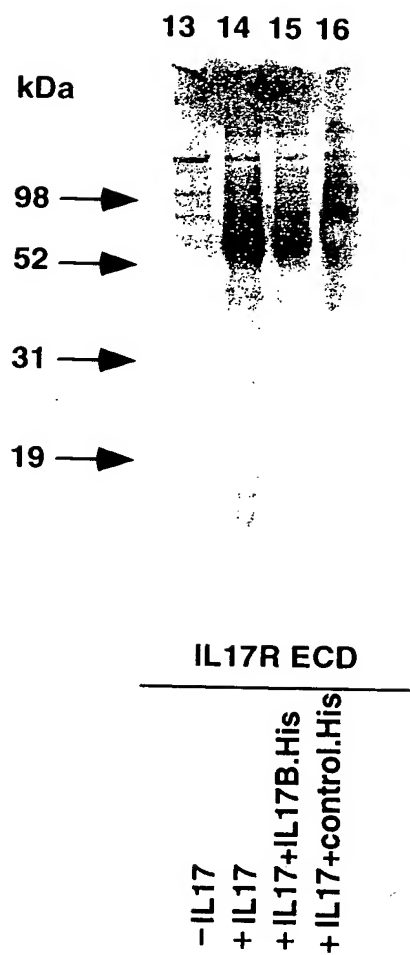


FIG. 29B

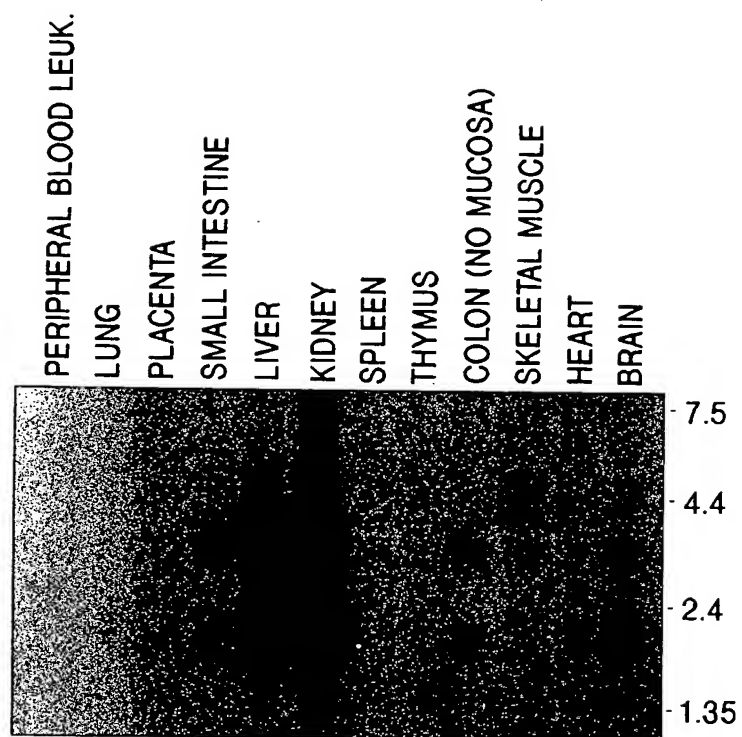


FIG. 31A

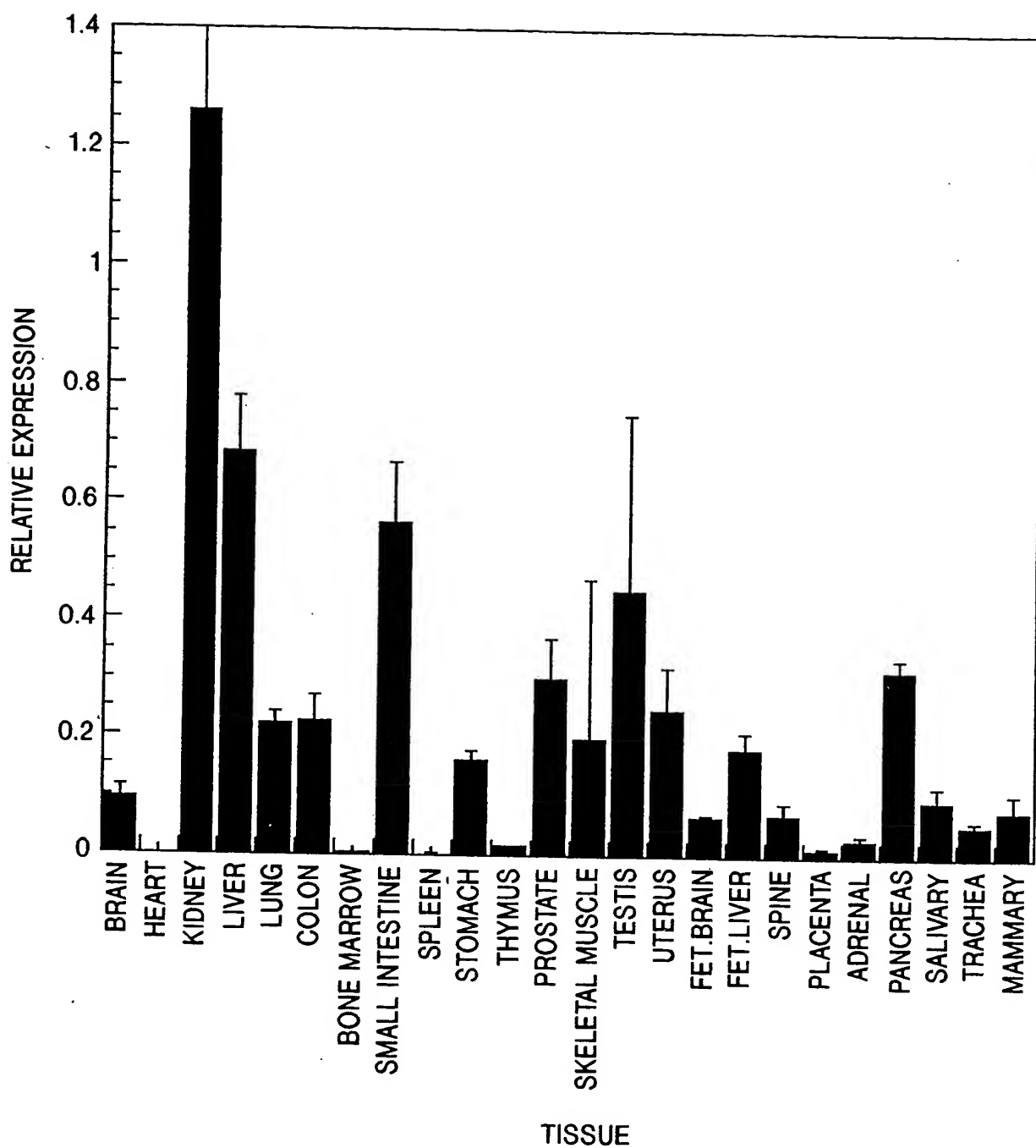


FIG. 31B

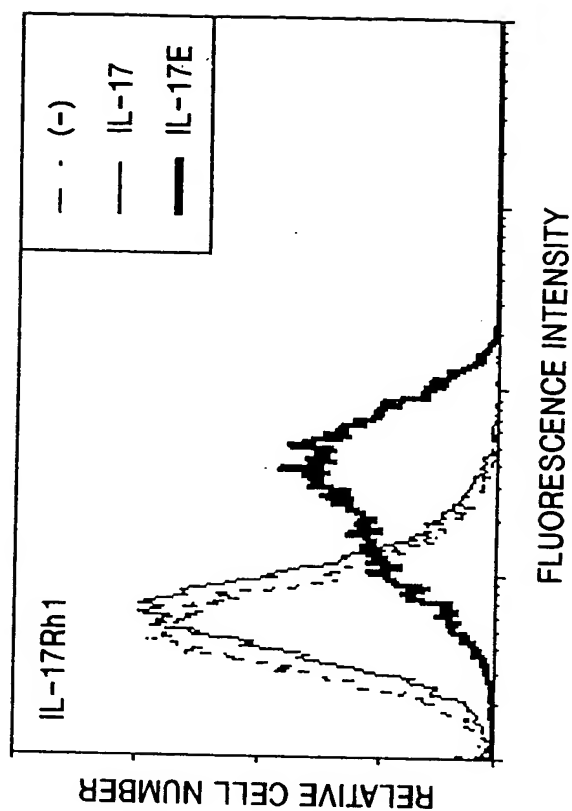
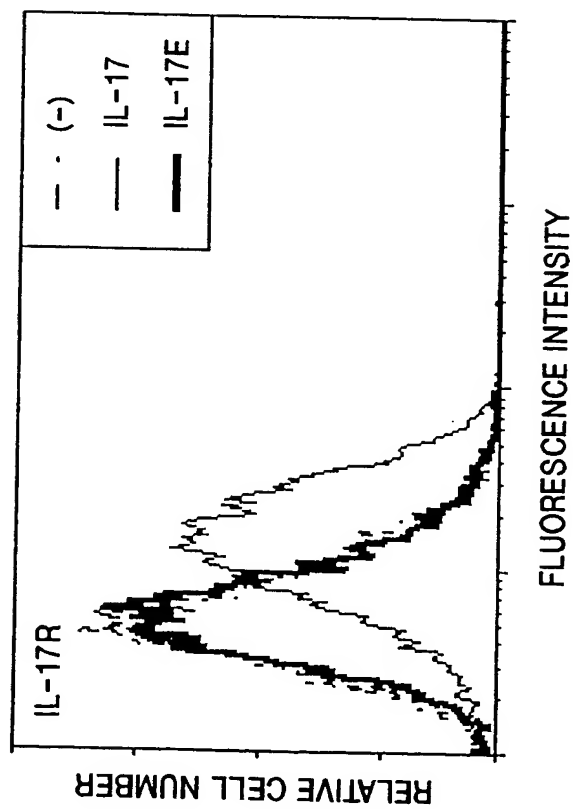


FIG. 32A

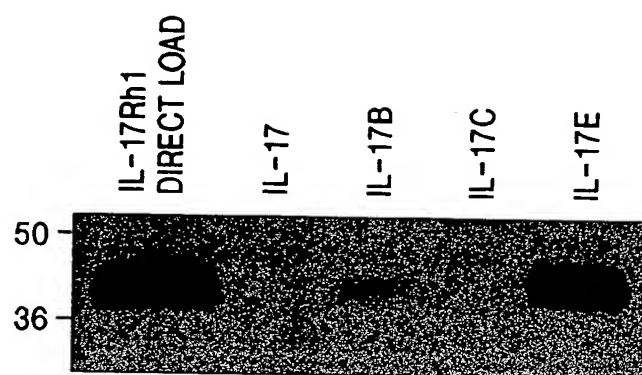


FIG. 32B

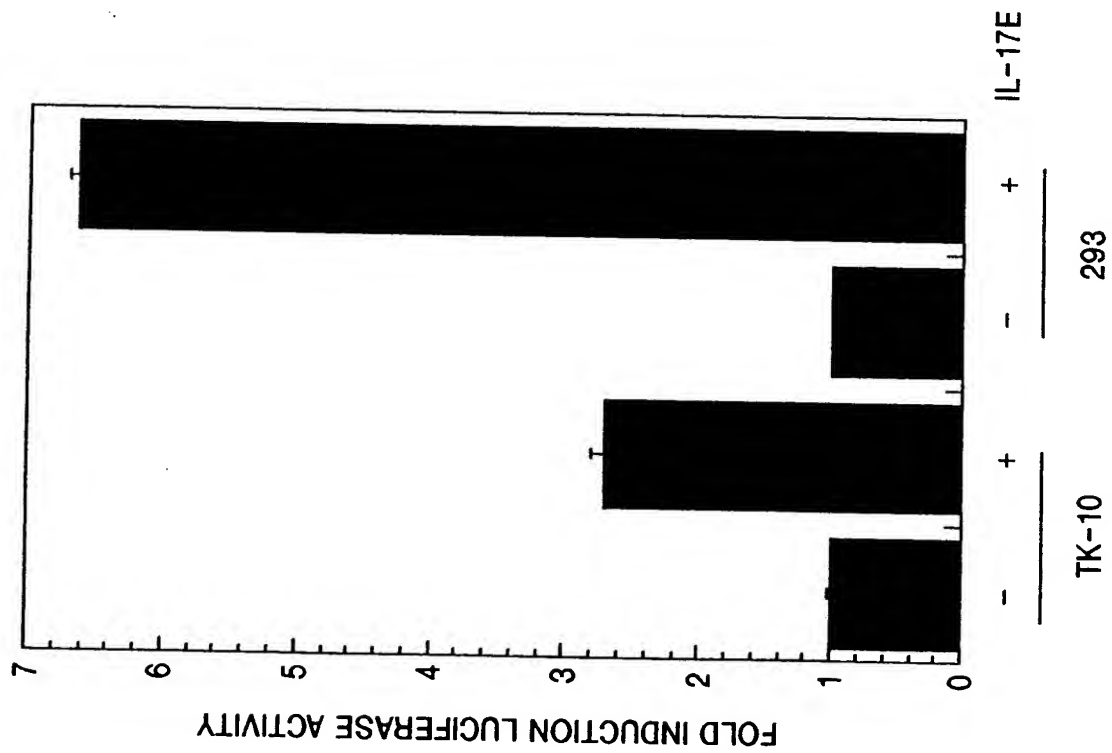


FIG. 33A

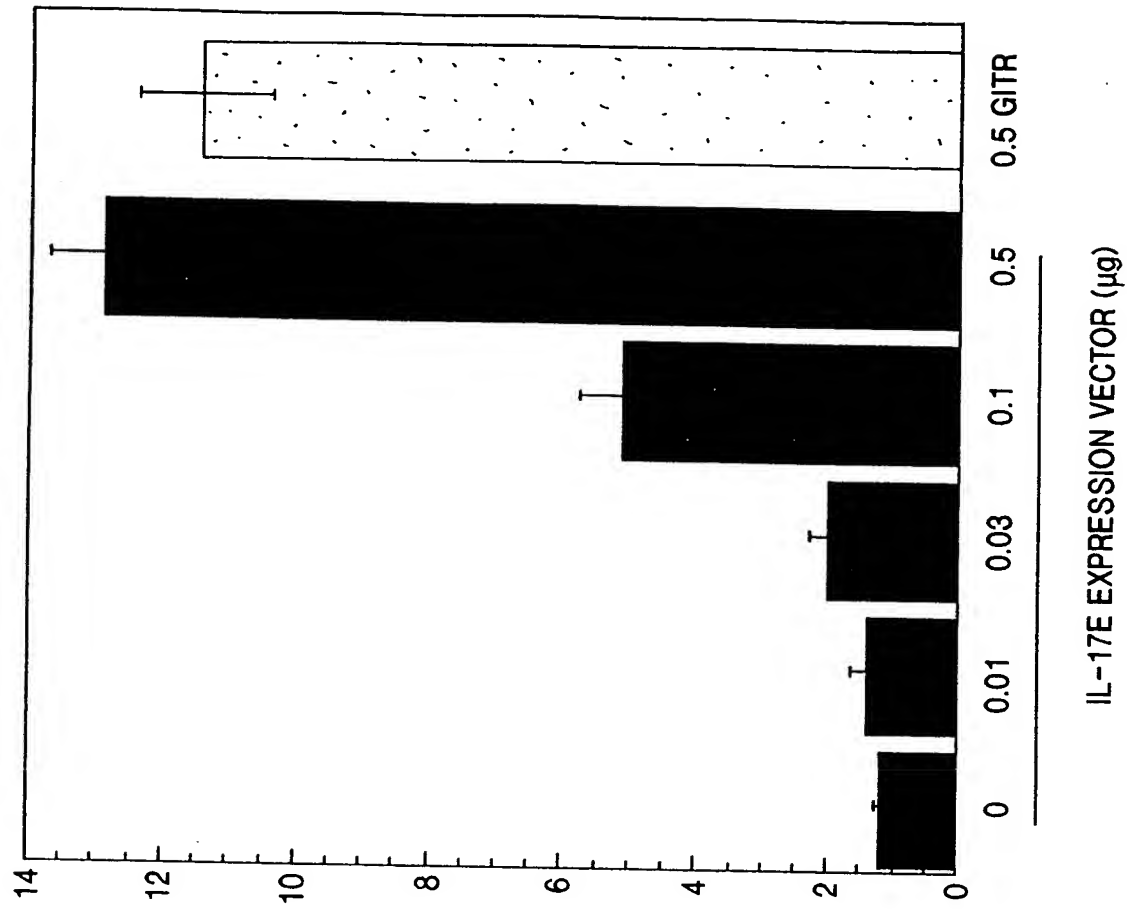


FIG. 33B

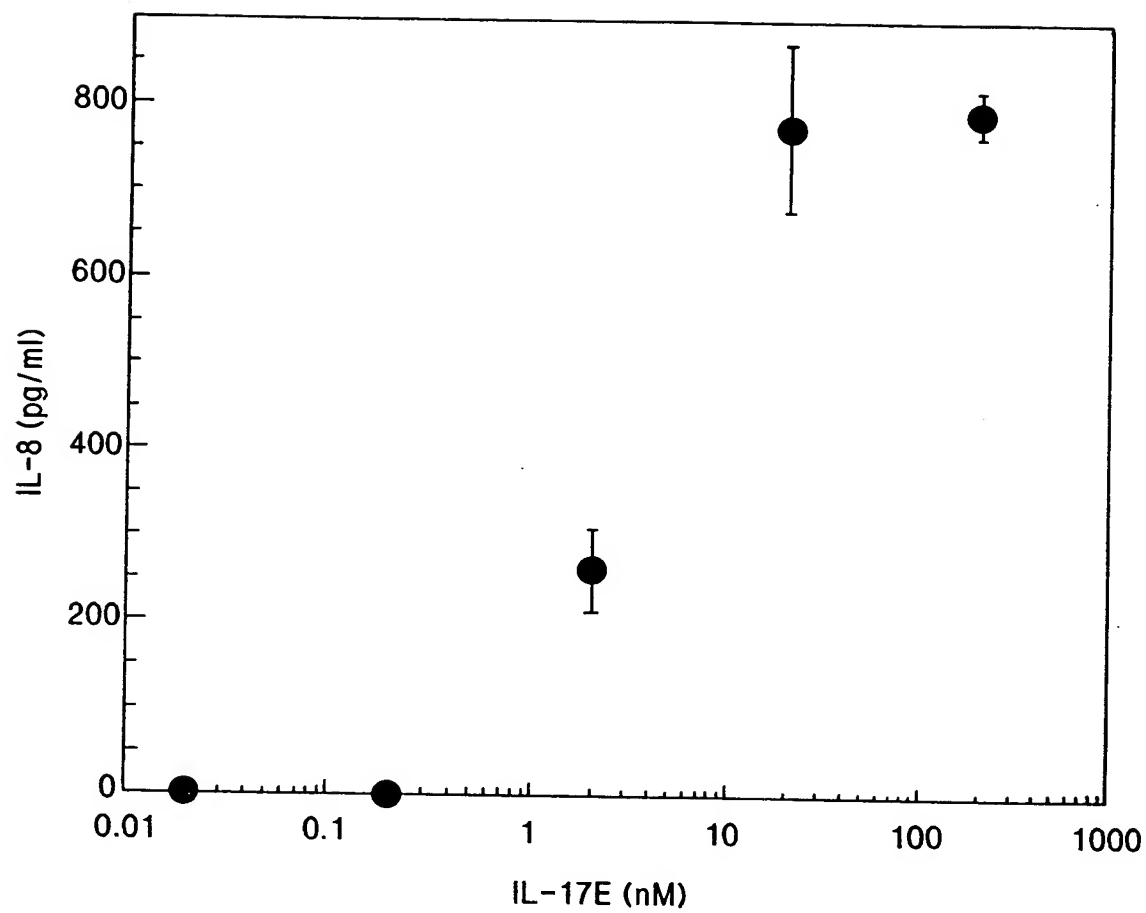


FIG. 34

IL-17 FAMILY OF CYTOKINES HAS COMPLEX PATTERN
OF OVERLAPPING RECEPTOR-LIGAND SPECIFICITIES

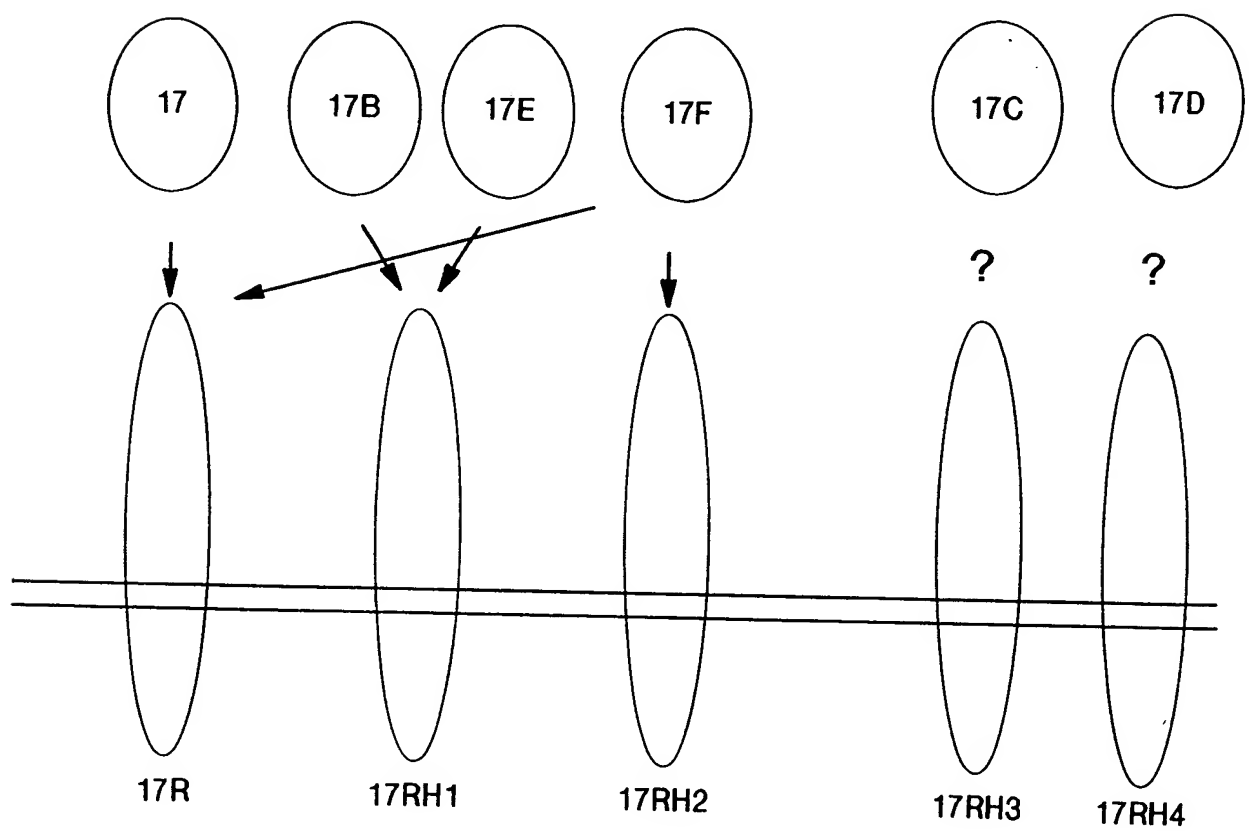


FIG. 35

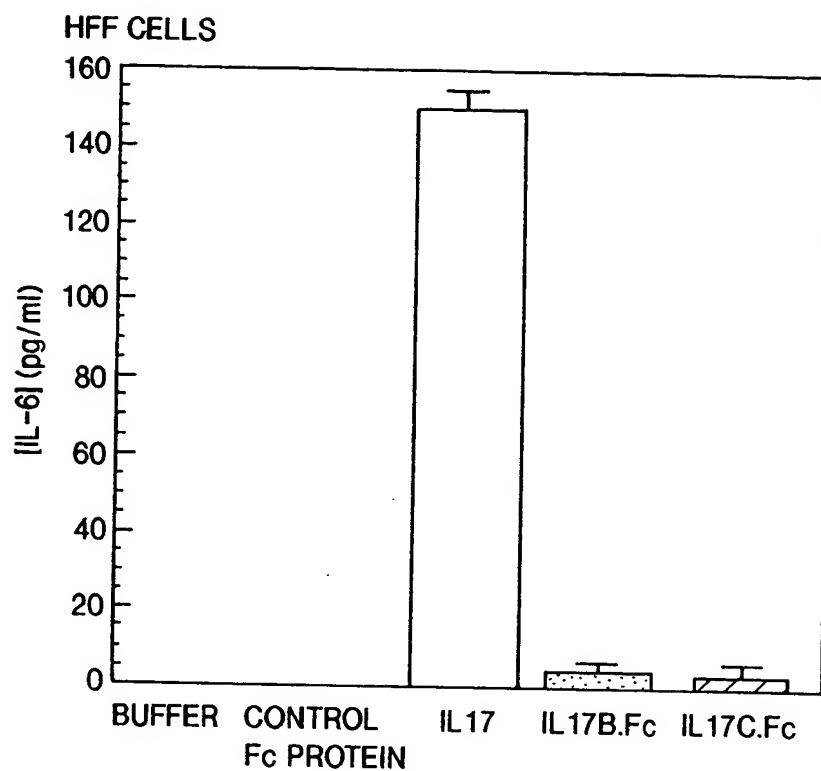


FIG. 36A

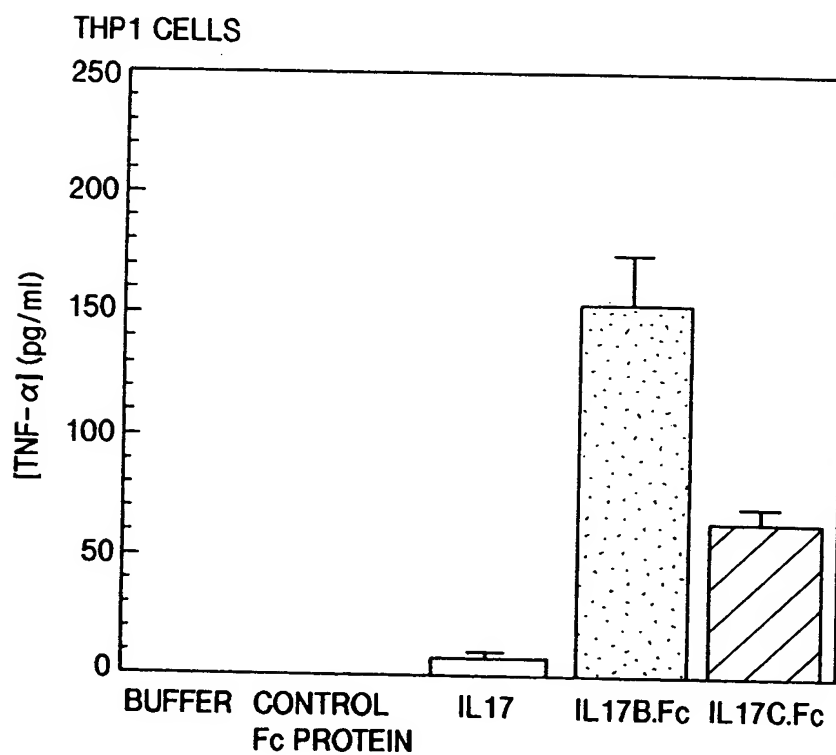


FIG. 36B

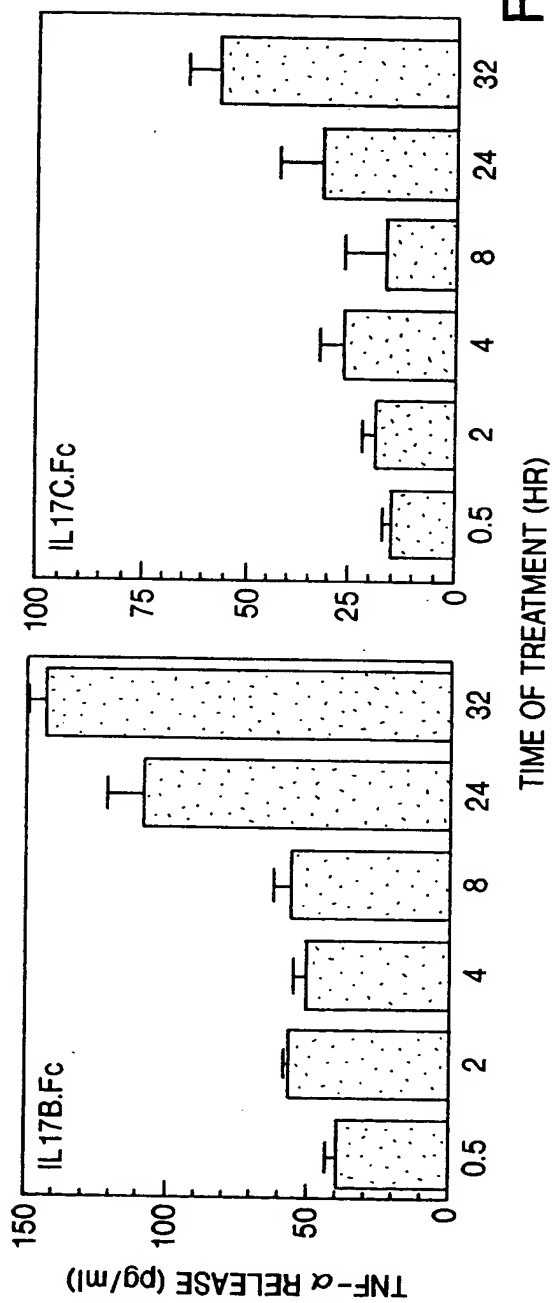


FIG. 37A

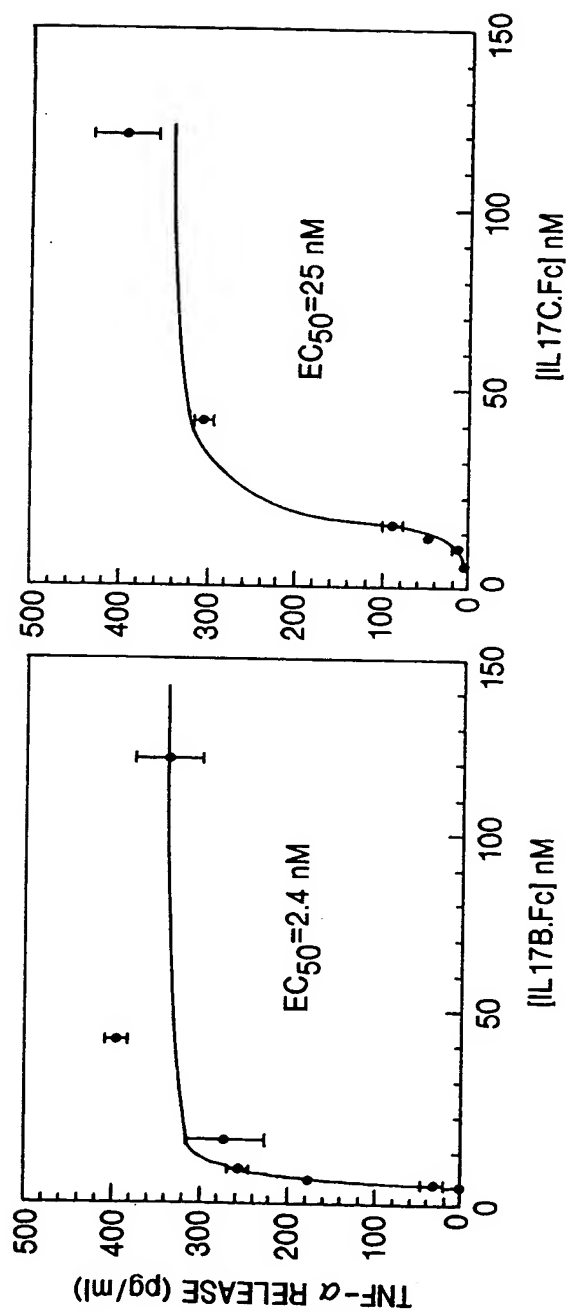


FIG. 37B

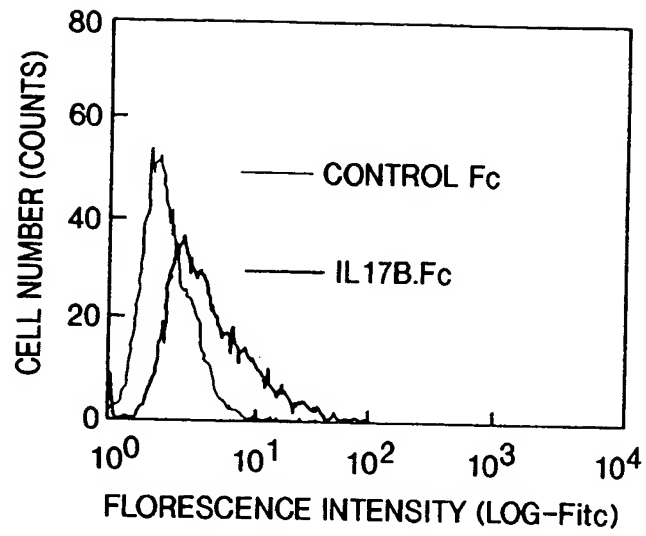


FIG. 38A

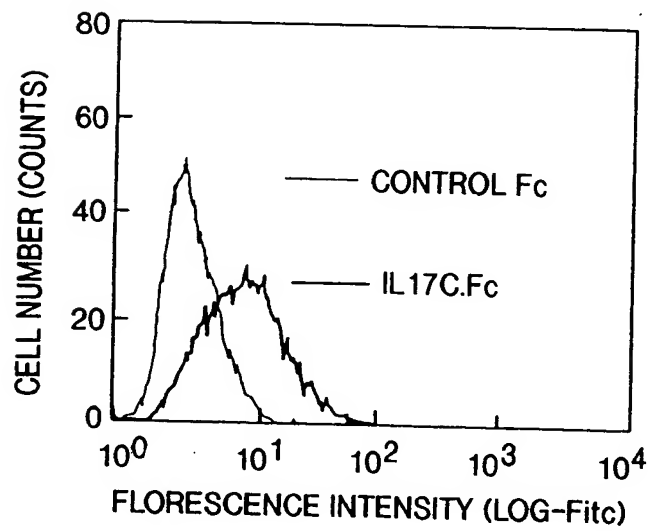


FIG. 38B

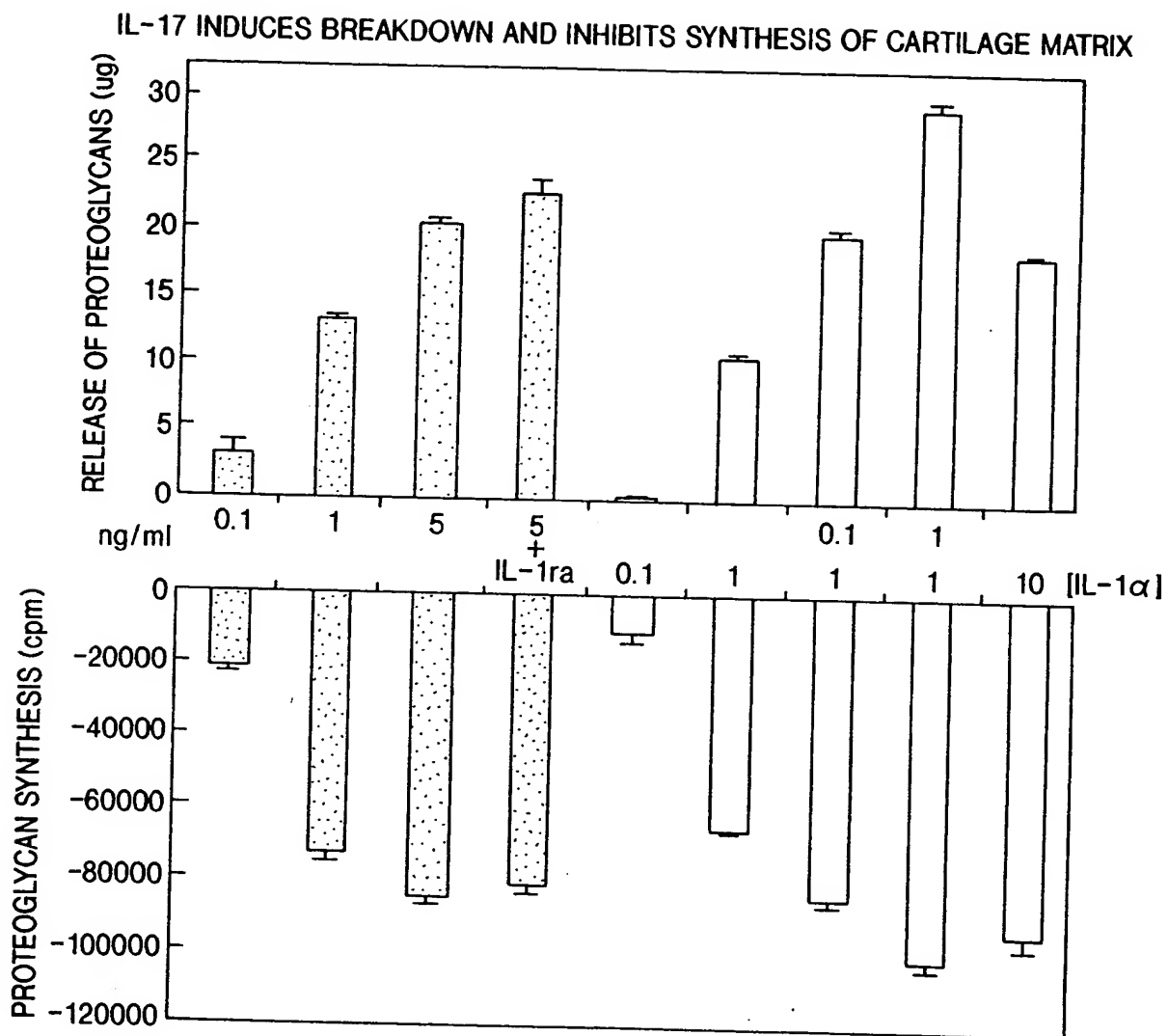


FIG. 39

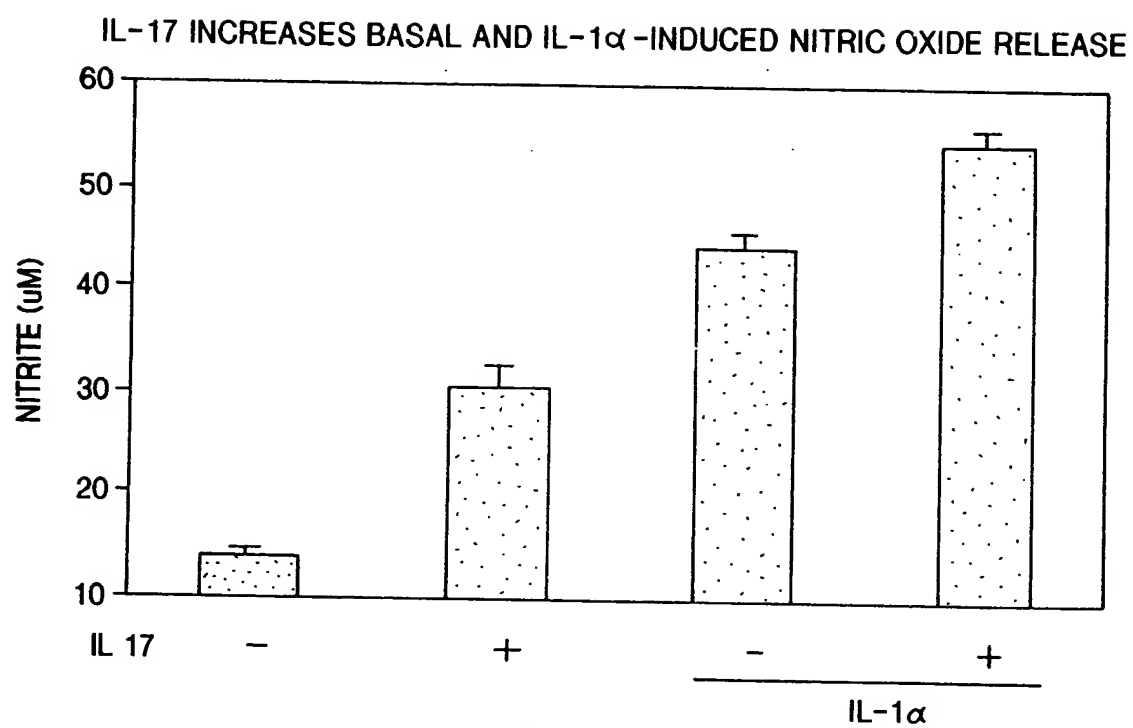


FIG. 40

INHIBITION OF NITRIC OXIDE RELEASE DOES NOT BLOCK THE DETRIMENTAL
EFFECTS OF IL 17 ON MATRIX BREAKDOWN OR SYNTHESIS

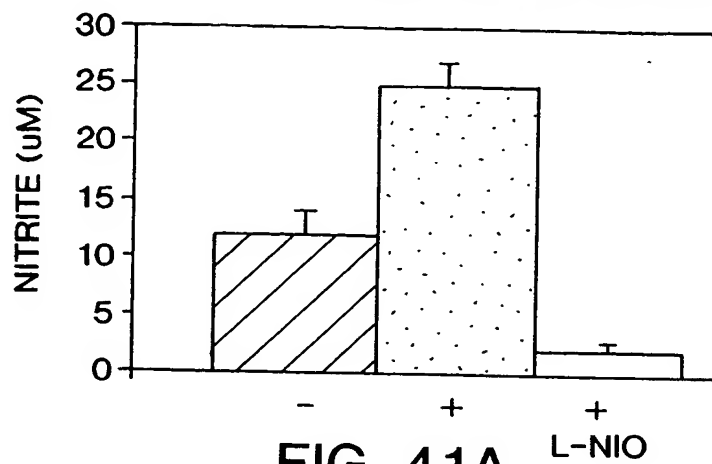


FIG. 41A

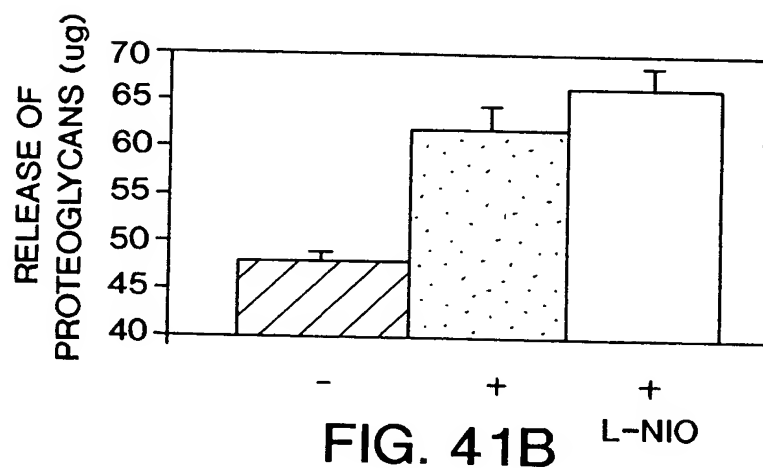


FIG. 41B

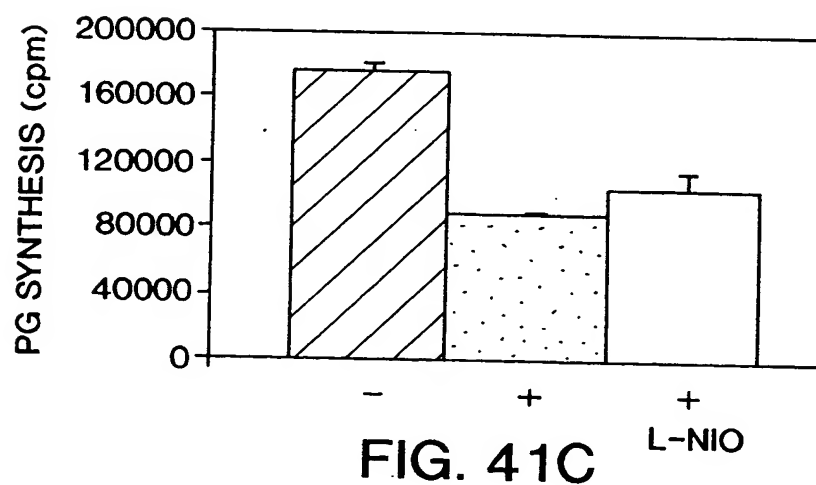


FIG. 41C

INHIBITION OF NO RELEASE ENHANCES IL1- α -INDUCED
MATRIX BREAKDOWN BUT NOT MATRIX SYNTHESIS

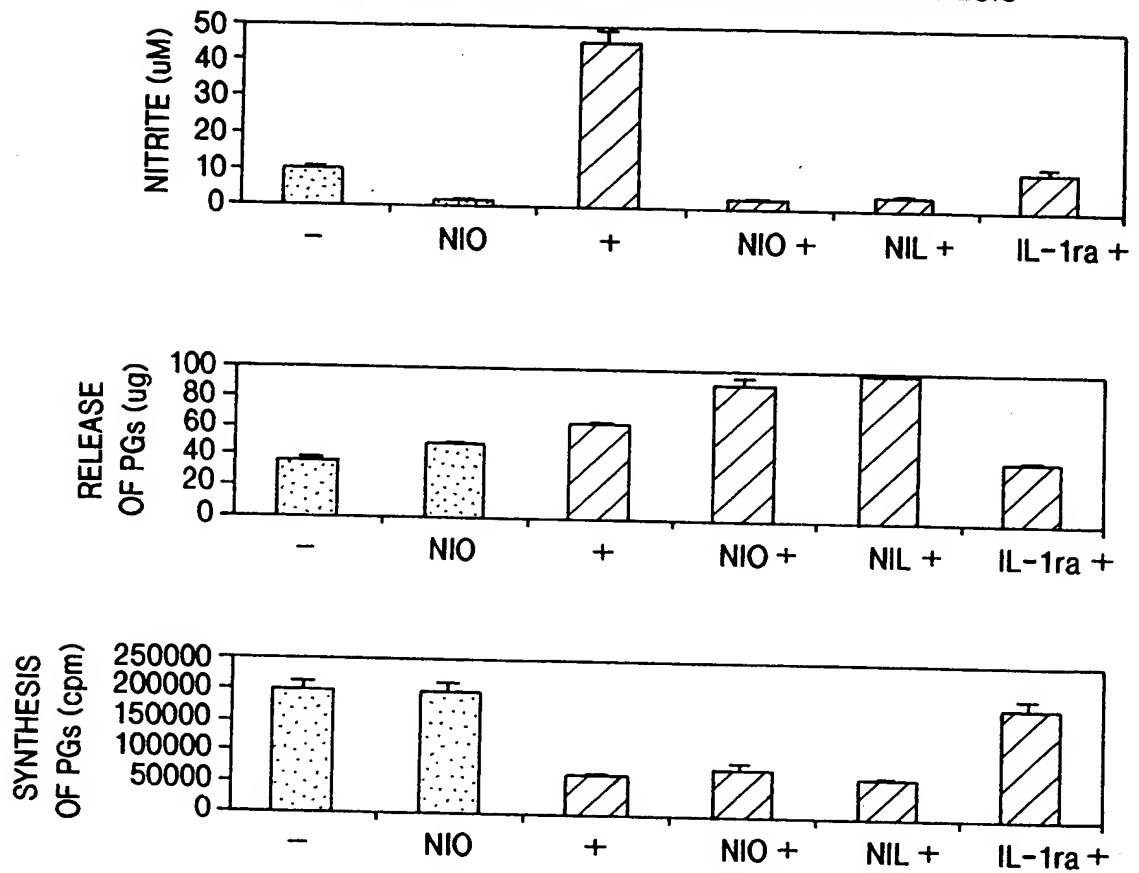


FIG. 42

IL-17C DETRIMENTAL EFFECTS ON ARTICULAR CARTILAGE

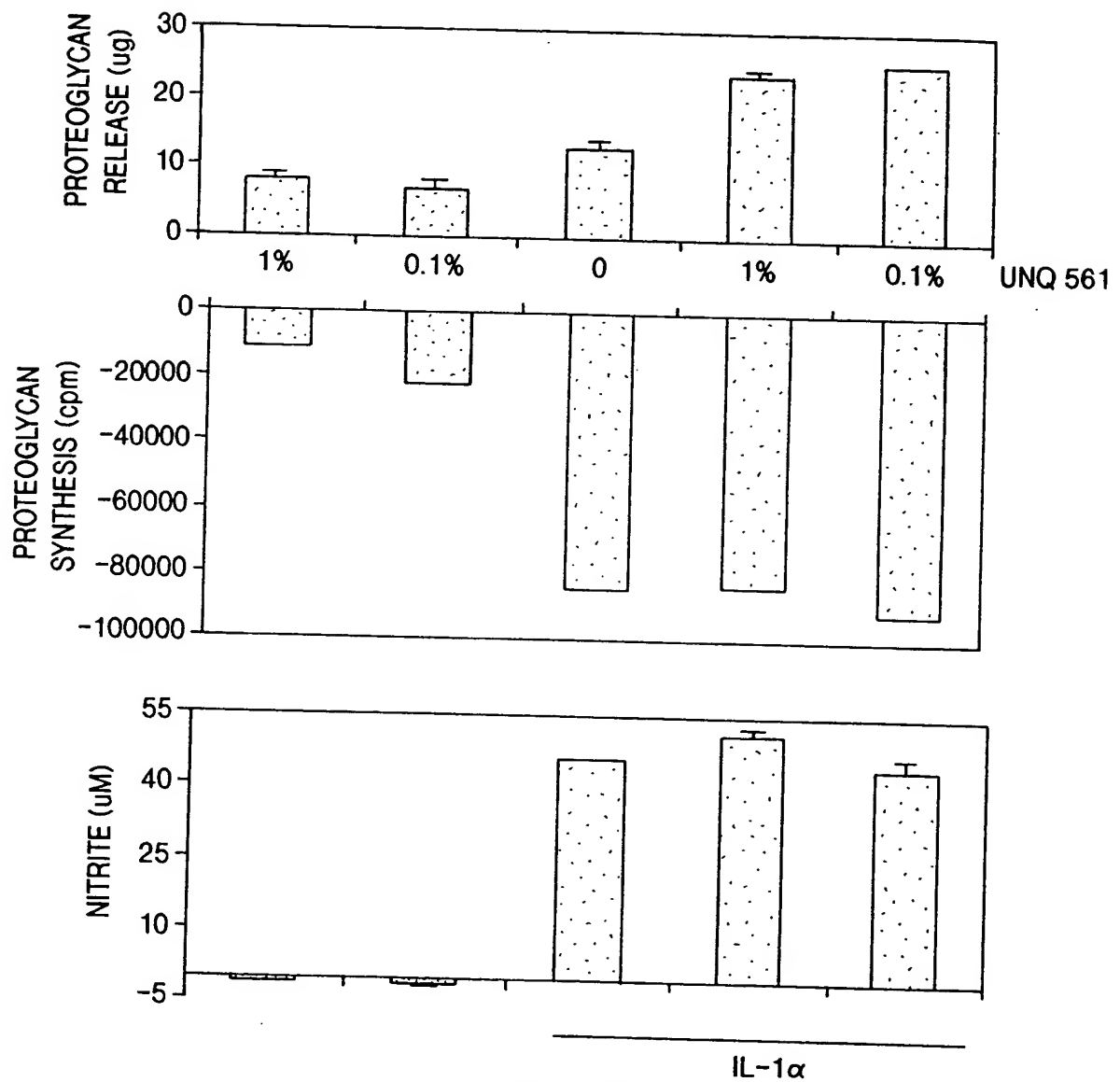


FIG. 43

INFLAMMATORY BOWEL DISEASE:
EXPRESSION OF IL-17 FAMILY IN MOUSE MODEL OF IBD

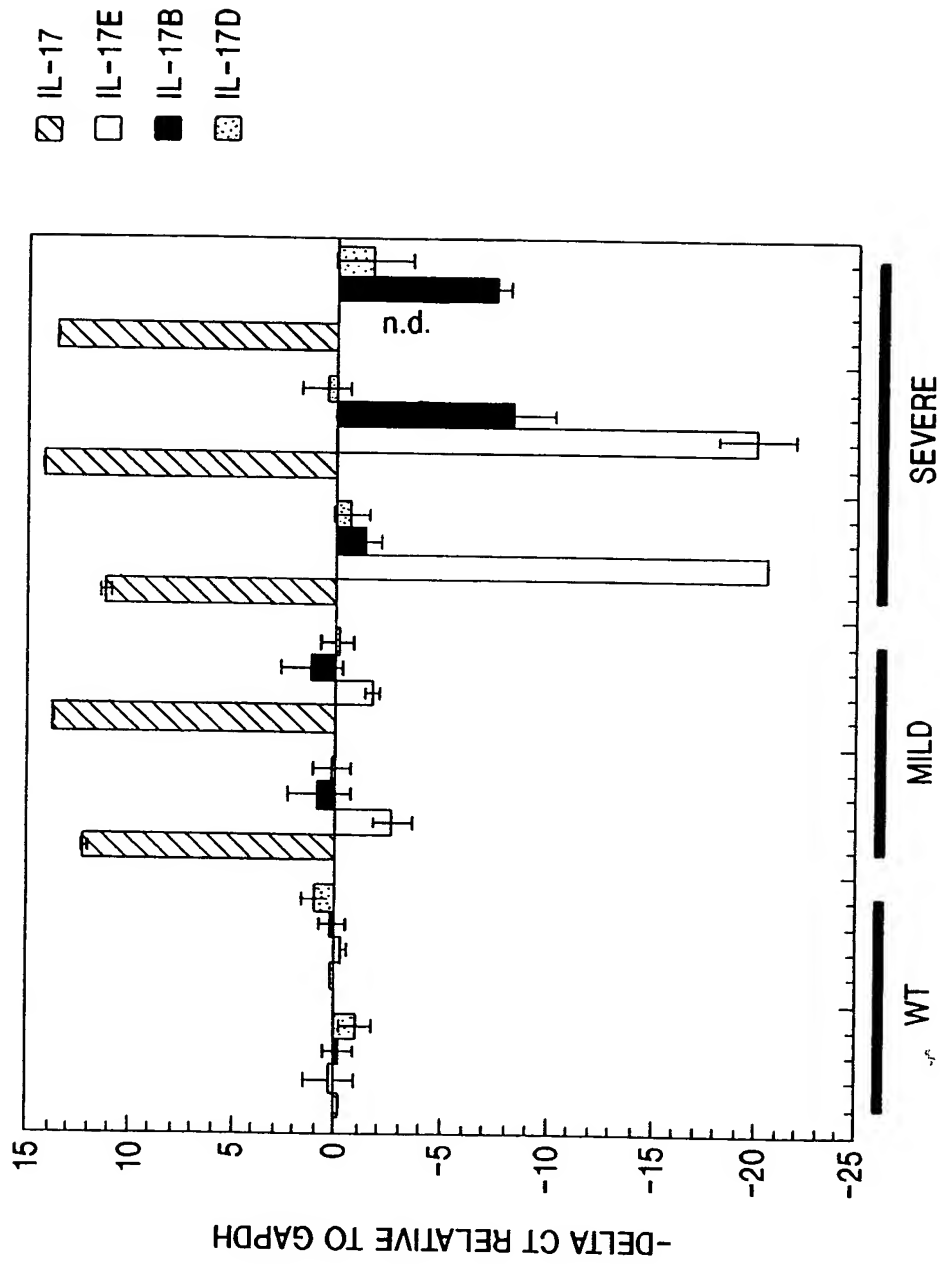


FIG. 44

IL-17D, PRESENT IN BRAIN, DECREASES RAPIDLY FOLLOWING STROKE

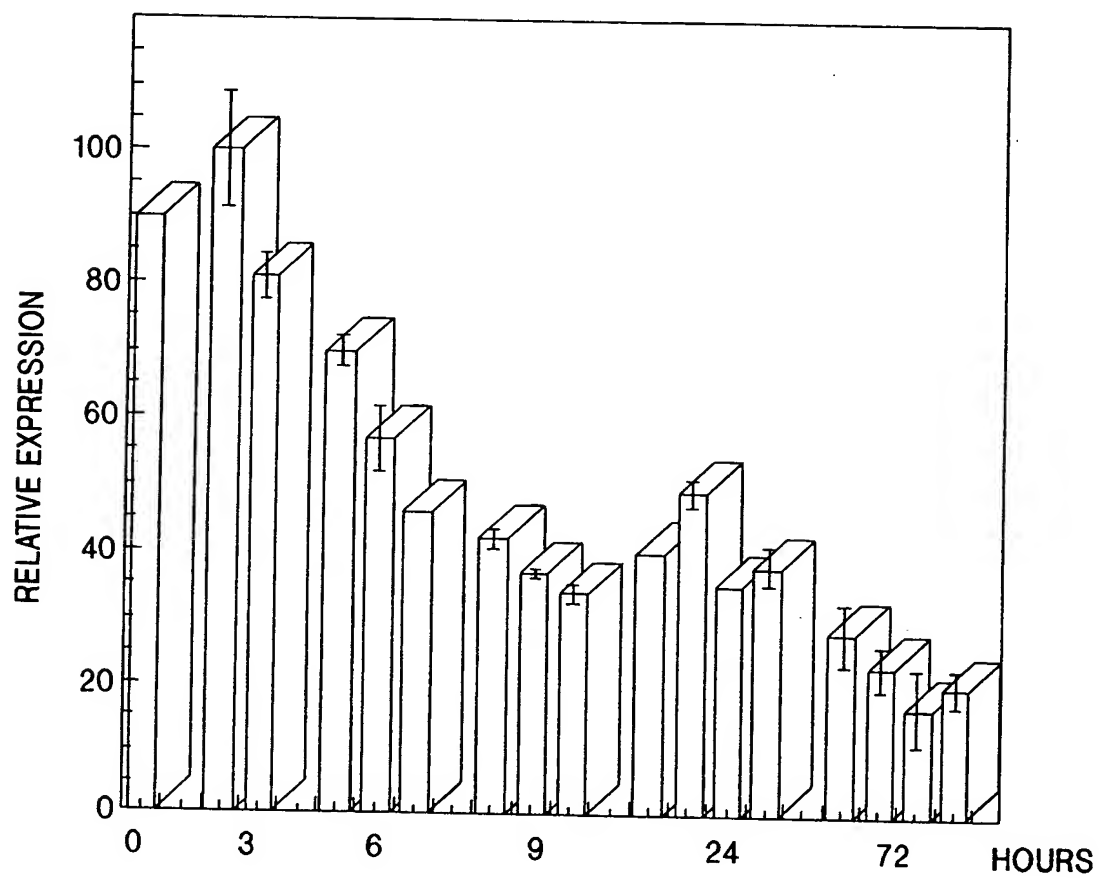


FIG. 45

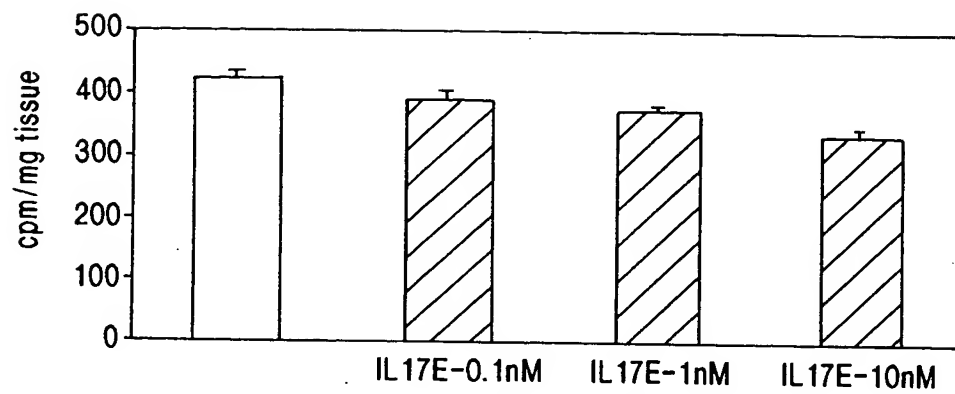


FIG. 46A

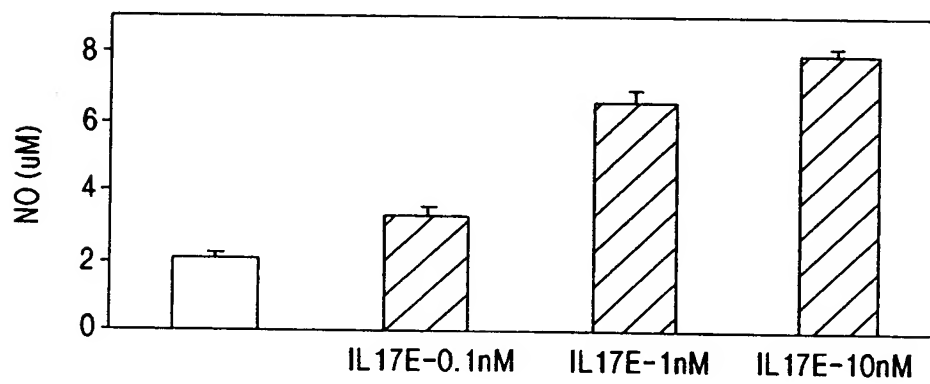


FIG. 46B

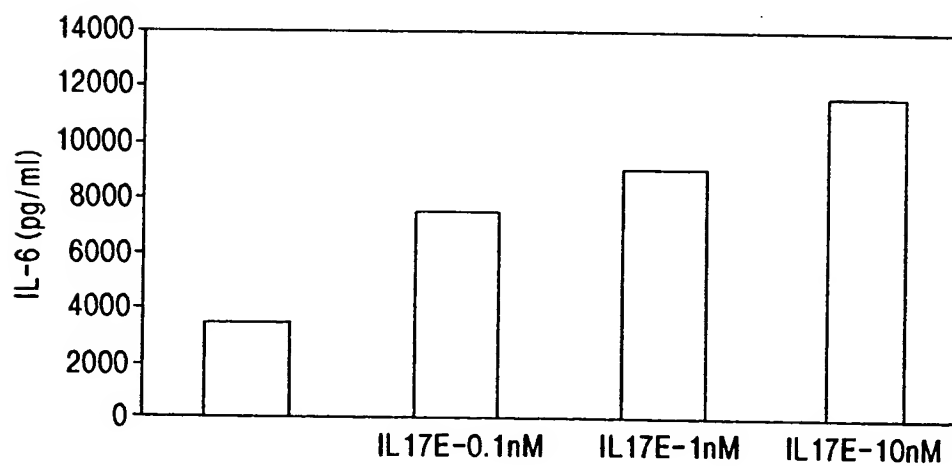


FIG. 46C

FIG. 47A

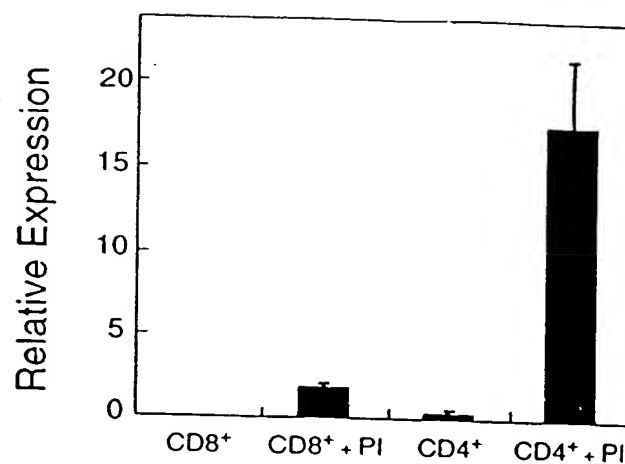


FIG. 47B

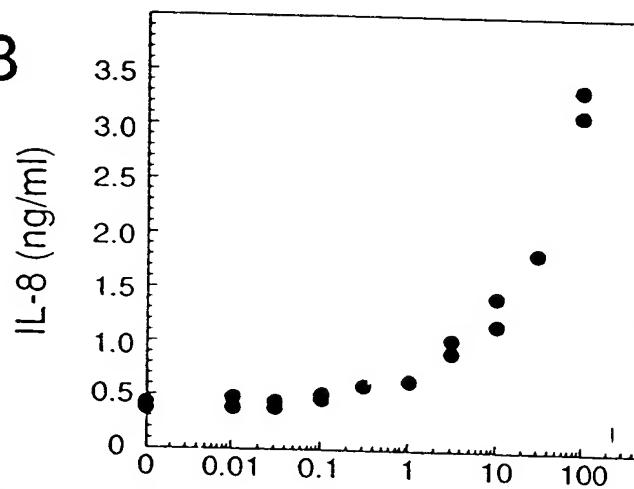
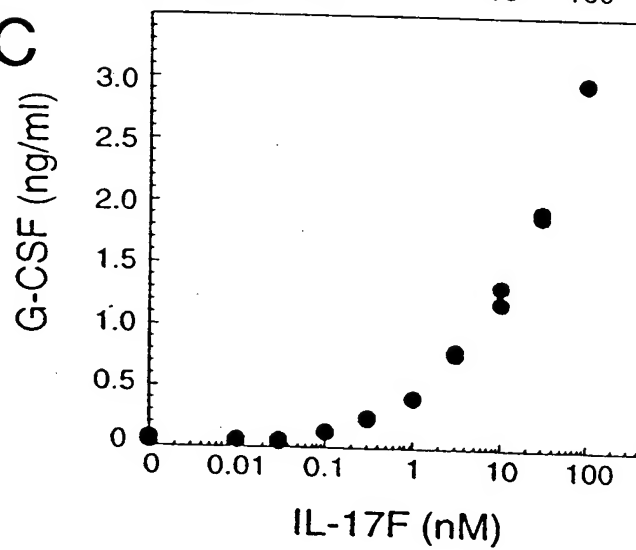


FIG. 47C



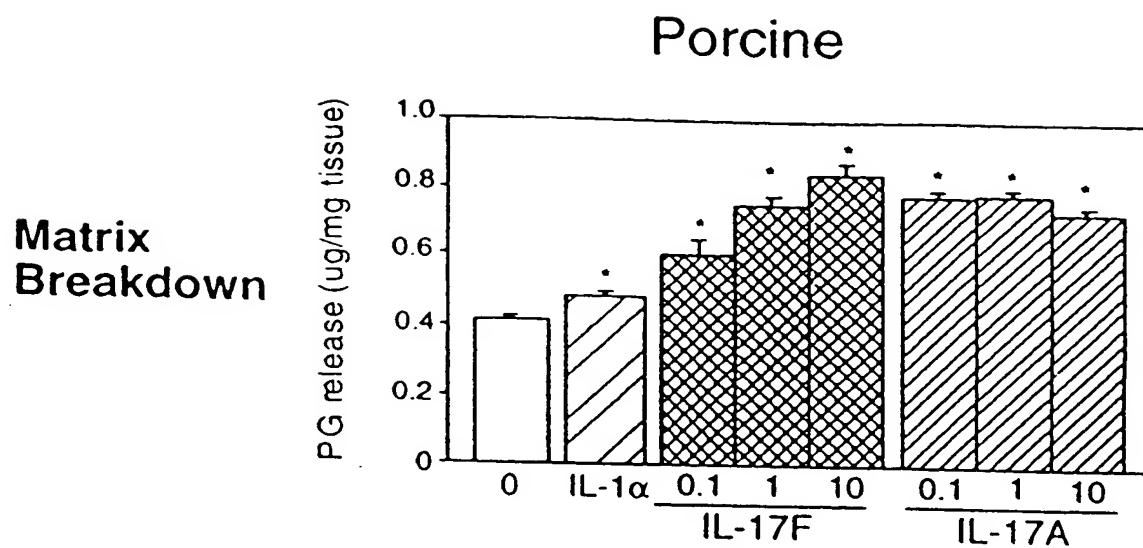


FIG. 48A

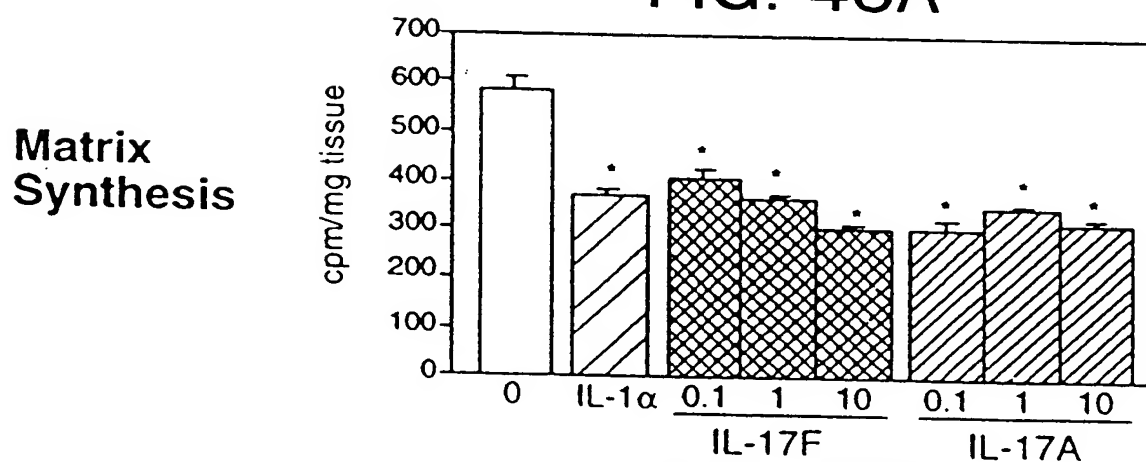


FIG. 48B

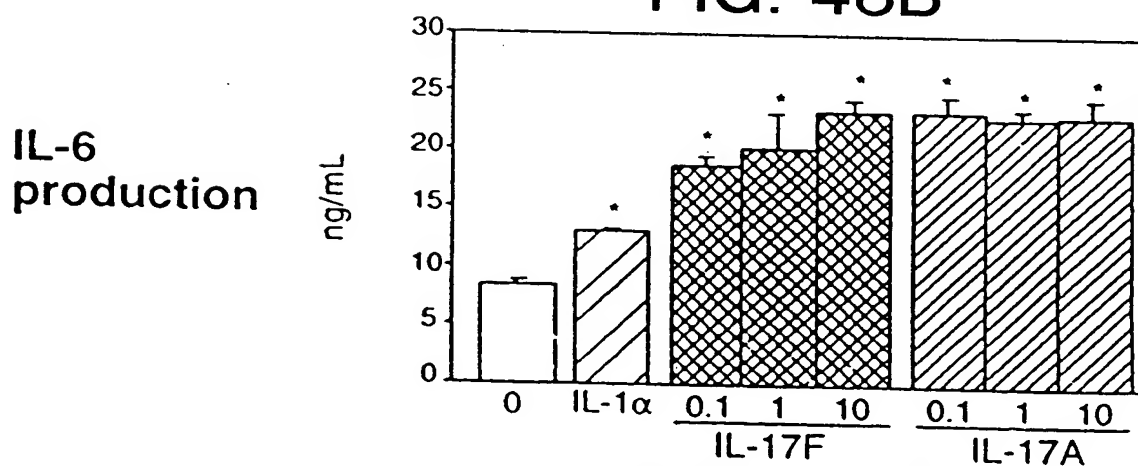


FIG. 48C

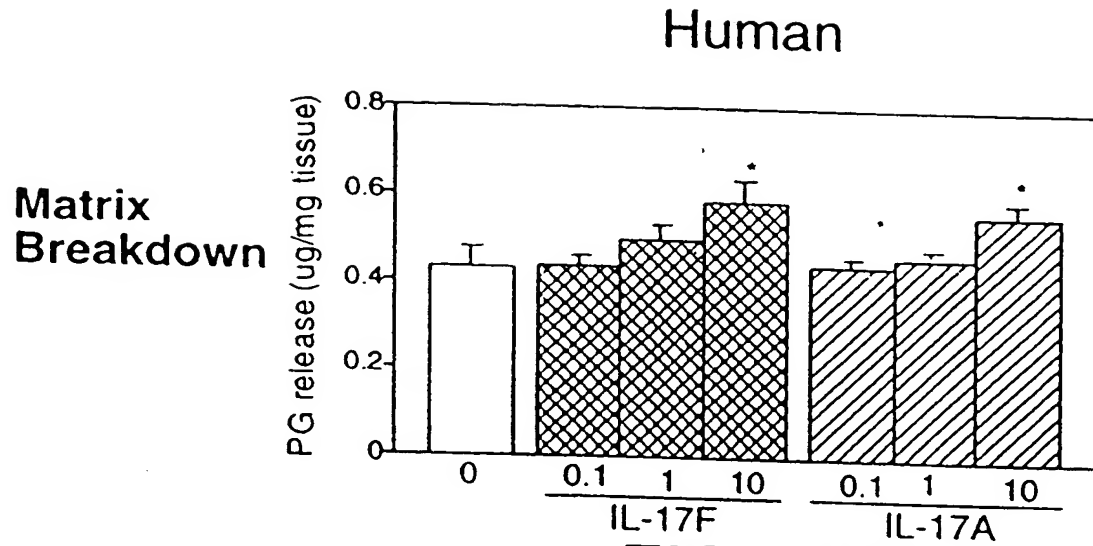


FIG. 48D

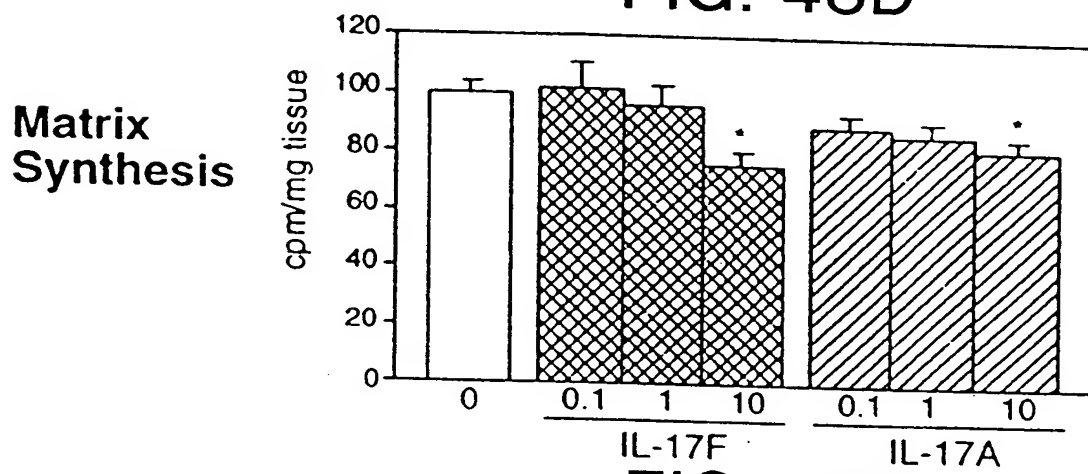


FIG. 48E

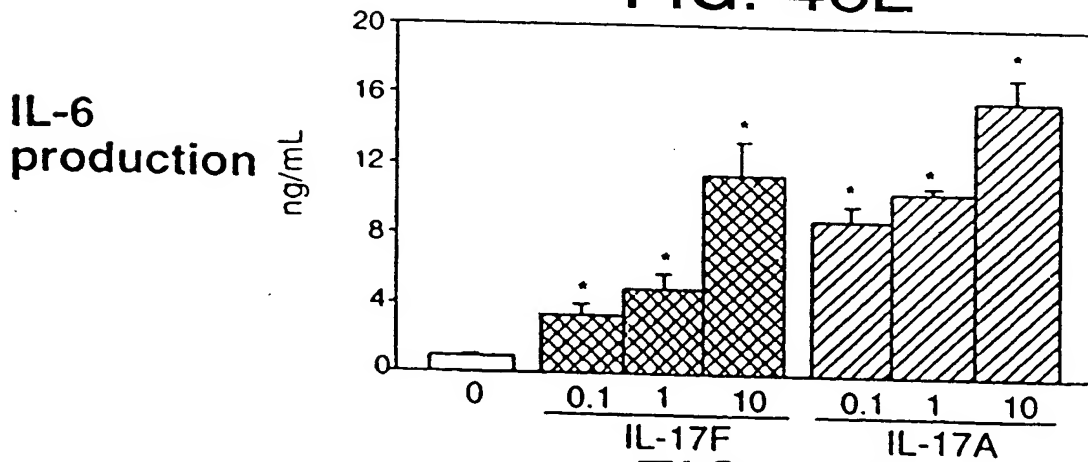


FIG. 48F

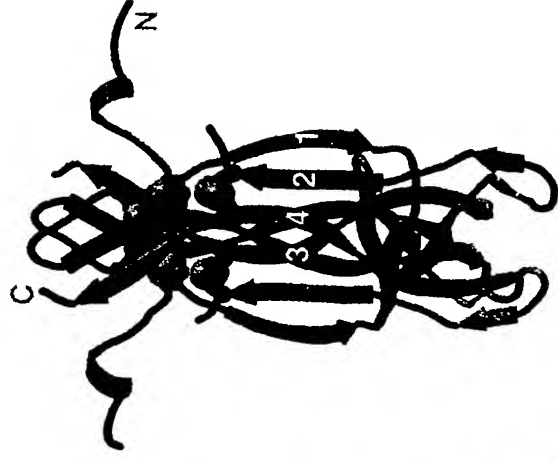
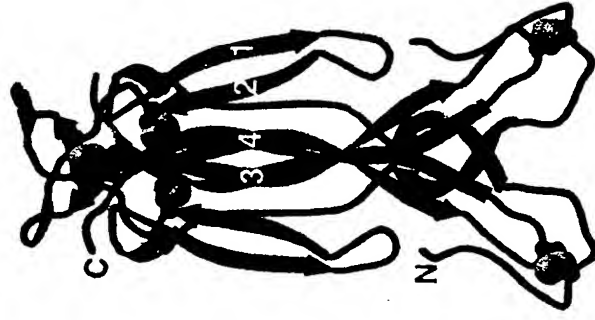
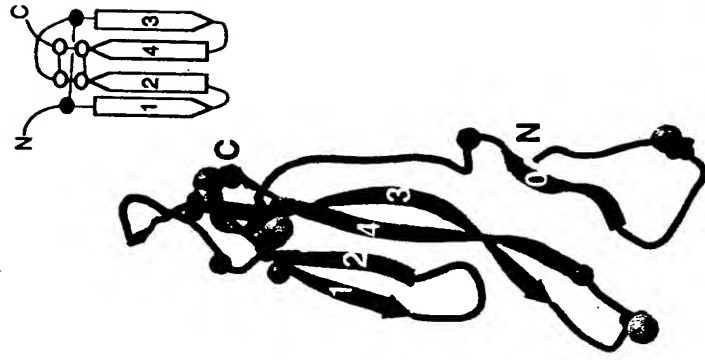


FIG. 49A

FIG. 49B

FIG. 49C

| | | | | | | | |
|--------|------------|-------------|------------|------------|------------|-----------|----|
| IL-17F | | | | | ...RKIPKVG | HTFFQKPES | 17 |
| IL-17A | | | | | ...TVKAG | ITIPRNP.G | 14 |
| IL-17B |QPRS | PKSKRKGQGR | PGPLAPGPHQ | VPLDLVSRMK | PYARMEEYER | | 44 |
| IL-17C | HHDPSLRGHP | HSHTGTPH.YS | AEELPLGQAP | PHLLARGAKW | GQALPVALVS | | 50 |
| IL-17E | | |YS | HWPS.PPSKG | QDTSEELLRW | | 22 |

| | | | | | | |
|--------|------------|------------|------------|------------|-----------|----|
| IL-17F | PPVPGG.... |SMKLDI | GIINENQRV | MSRNIESRST | PWNYTVTWD | 59 |
| IL-17A | PNSDKNFPR | TVMVNLNIHN | RNTNTN..PK | RSDYYNRST | PWNLHRNED | 62 |
| IL-17B | NIEEMVAQLR | ..NSSELAQR | KCEV....NL | QLWMSNKRSL | PWGYSINHD | 88 |
| IL-17C | SLEAASHRGR | ..HERPSATT | Q.PVLRPEEV | LEADTHQBSI | PWRYRVDTD | 98 |
| IL-17E | STVPVPPLP | ..ARPNRHPE | S.RASE.... | .DGPLNSRAI | PWRYELDRD | 65 |

| | | | | | | |
|--------|------------|------------|------------|------------|----------------|-----|
| IL-17F | PNRYPSEVVQ | AQ.RNLG-IN | A..QGKEDIS | MN.VPI.QQE | TLVVRKHKQG | 106 |
| IL-17A | PERYPVIWE | AK.RHLG-IN | A..DGNVDYH | MN.VPI.QQE | ILVLRREPPH | 109 |
| IL-17B | PSRIEVDLPE | AR.LGLG-VN | PF.TMQEDRS | MV.VPV.FSQ | VPVRRR...L | 133 |
| IL-17C | EDRYPQKLAF | AE.L.RG-ID | AR.TGRETA | LN.VRL.LQS | LLVLR...RP | 144 |
| IL-17E | LNRLPQDLYH | AR.L.PH-VS | LQTGSHMDPR | GN.ELLYHNQ | TVFYRRP... 112 | |

| | | | | | | |
|--------|-------------|------------|------------|------------|-----|-----|
| IL-17F | CSV..... |SFQLEK | VL..VTUGCT | CMTFVIHHVQ | ... | 133 |
| IL-17A | CPN..... |SFRLEK | IL..VSVGCT | CMTFIVHHVA | ... | 136 |
| IL-17B | CPPPRTGP. |CRQRA | VMTIAGCT | CIF..... | ... | 160 |
| IL-17C | CSRDGSGLEPT | PGAFATHTF | IH..VPVGT | CV.LPRSVAA | ALE | 184 |
| IL-17E | CHGEKGTHKG |YCLER | RLYRVSLACV | CVRPRVMG.. | ... | 145 |

FIG. 50

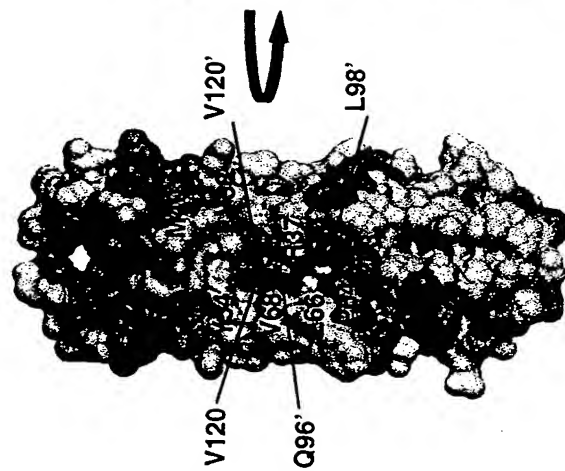


FIG. 51A

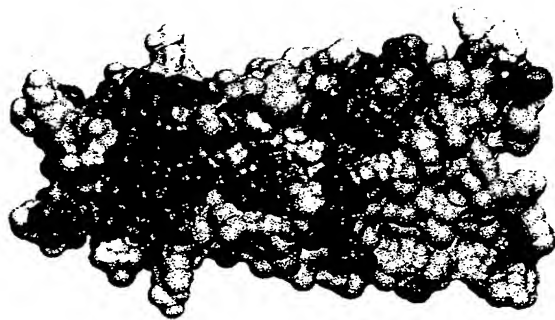


FIG. 51B

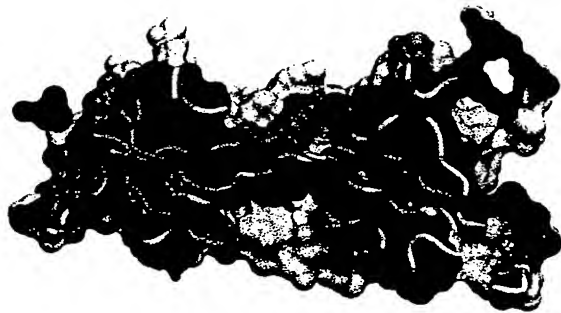


FIG. 51C

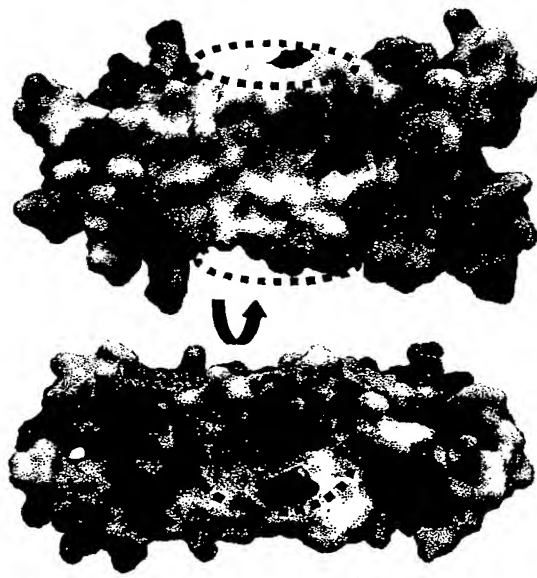


FIG. 52A

FIG. 52B

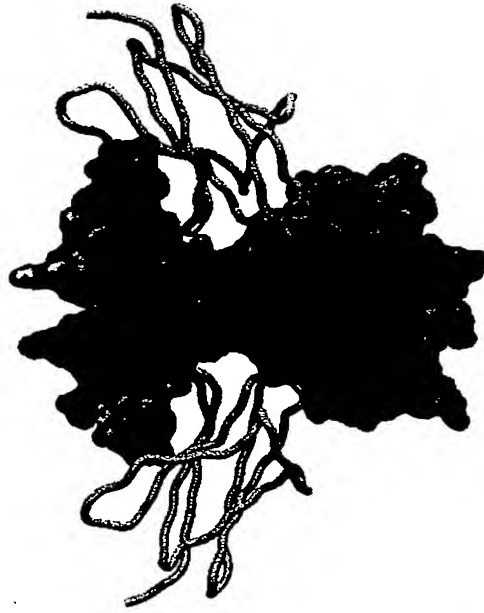
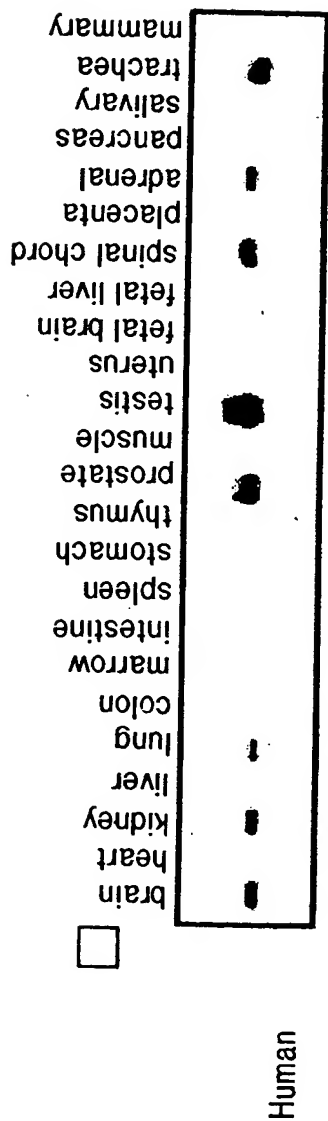


FIG. 52C

| | | | | | | | | |
|--------|-----|---------------------|------------|----------|-------|------------|------|----------------|
| mL-17E | 1 | - - - - - | VAFLAM | IV | GTH | TVSLRIQEGC | SHL | PSCCCPS |
| nL-17E | 1 | MRERPRLGEDSSLSIFLQV | VAFLAM | VM | GTH | T | YSHW | PSCCCPS |
| mL-17E | 35 | KEQEPPEWLKWS | SASVSPP | EPL | SHTHA | ESCRA | SKDG | PLNSRAISPWYS |
| nL-17E | 43 | KGQDTS EELLRWS | TVPV PPL | EPARP | NRHHP | ESCRA | SEDE | GPLNSRAISPWR Y |
| mL-17E | 85 | ELDRDLNRVLPQDDL | YHARCLCPHC | VS LQTGS | HMDPL | GNSVP | LYHN | QTVFYR |
| nL-17E | 93 | ELDRDLNRLLPQDDL | YHARCLCPHC | VS LQTGS | HMDPR | GNS EL | LYHN | QTVFYR |
| mL-17E | 135 | RPCHGEETGTHR | RRYCLERR | LYRVSLAC | VCVR | PRVMA | | |
| nL-17E | 143 | RPCHGEKGTH | KGYCLERR | LYRVSLAC | VCVR | PRVMG | | |

FIG. 53

Tissue distribution of IL-17E



IL-17E (PCR then probed with cDNA)

FIG. 54B

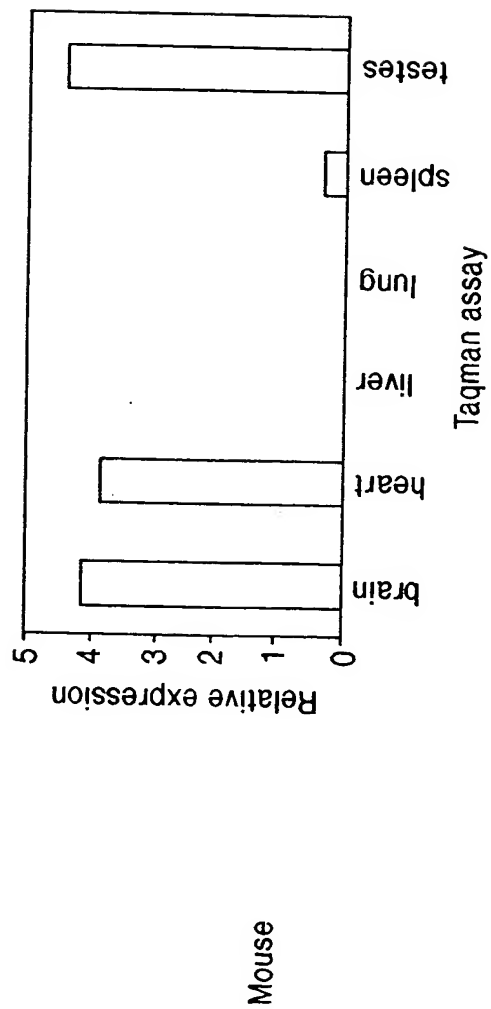


FIG. 54A

mIL-17E transgenics are growth retarded

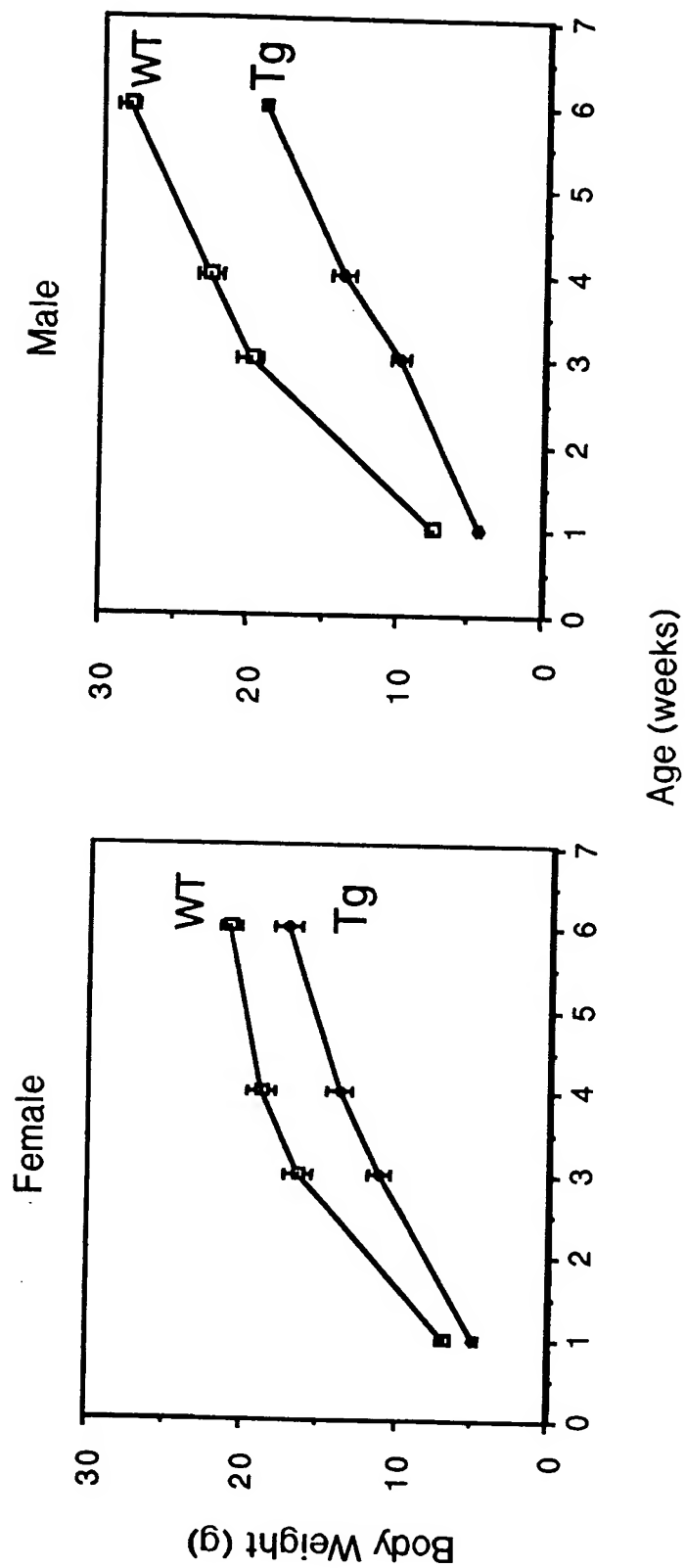


FIG. 55

IL-17E transgenics are jaundiced by 6 weeks of age



FIG. 56

mIL-17E transgenics have elevated total bilirubin and liver enzymes

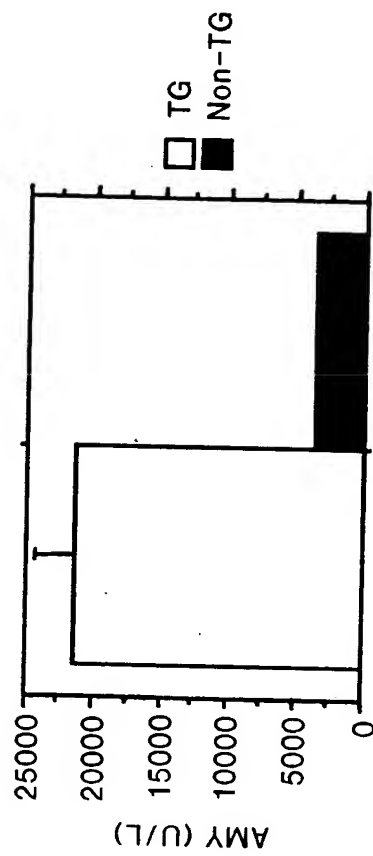
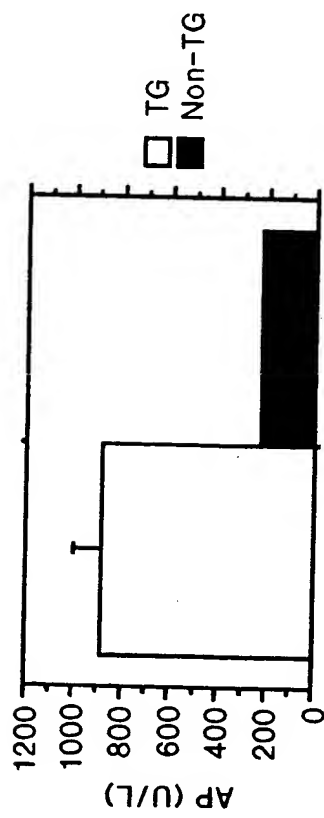
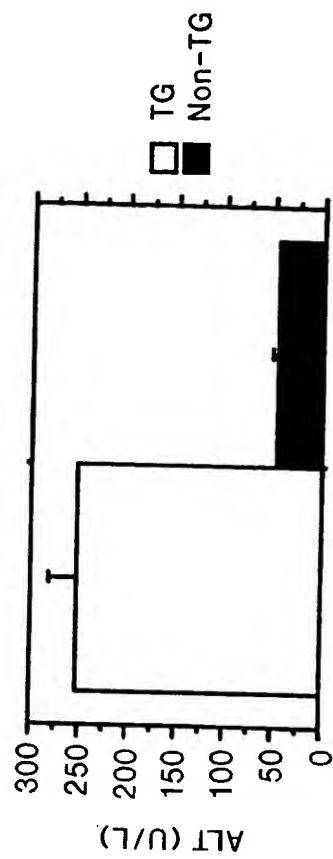
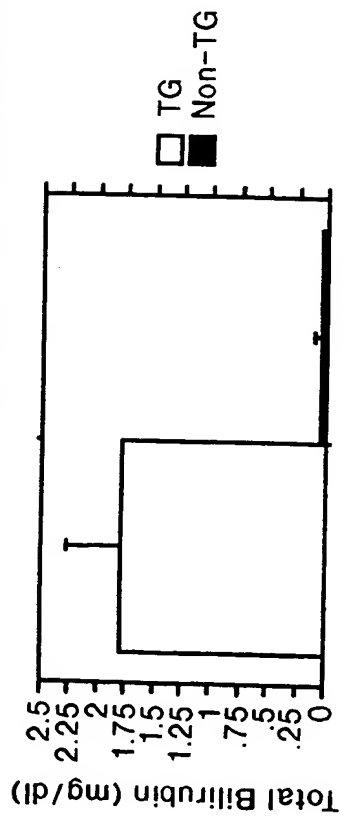


FIG. 57

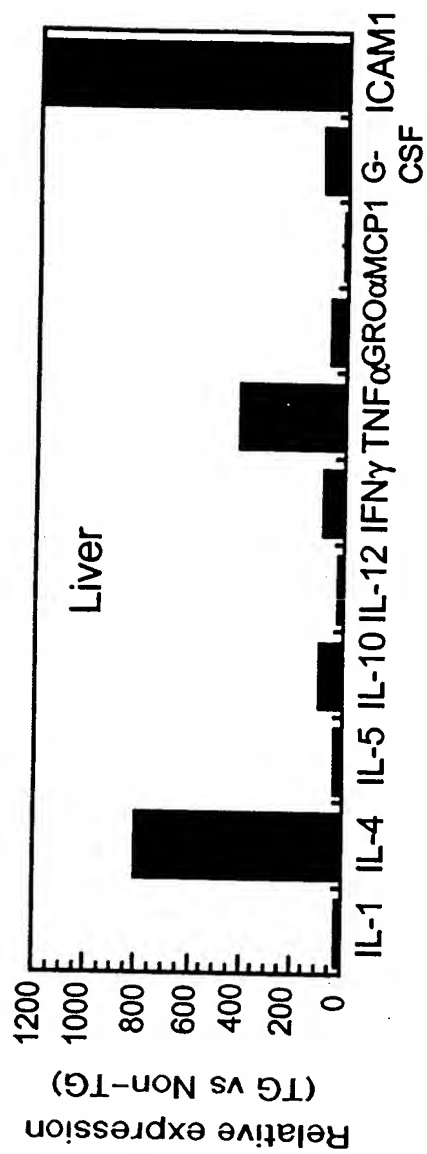


FIG. 58A

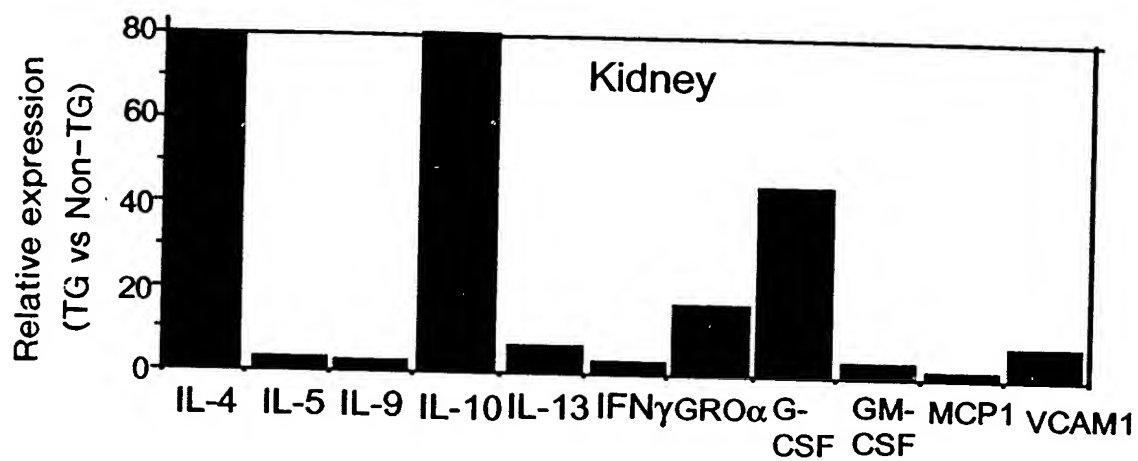


FIG. 58B

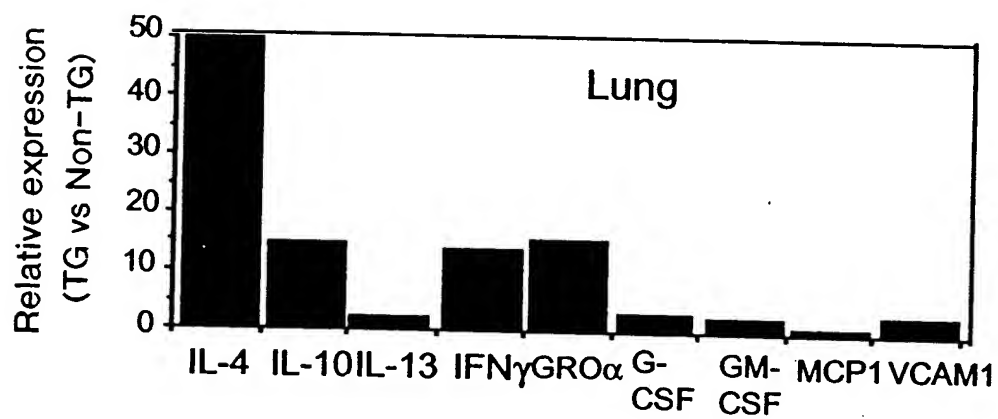
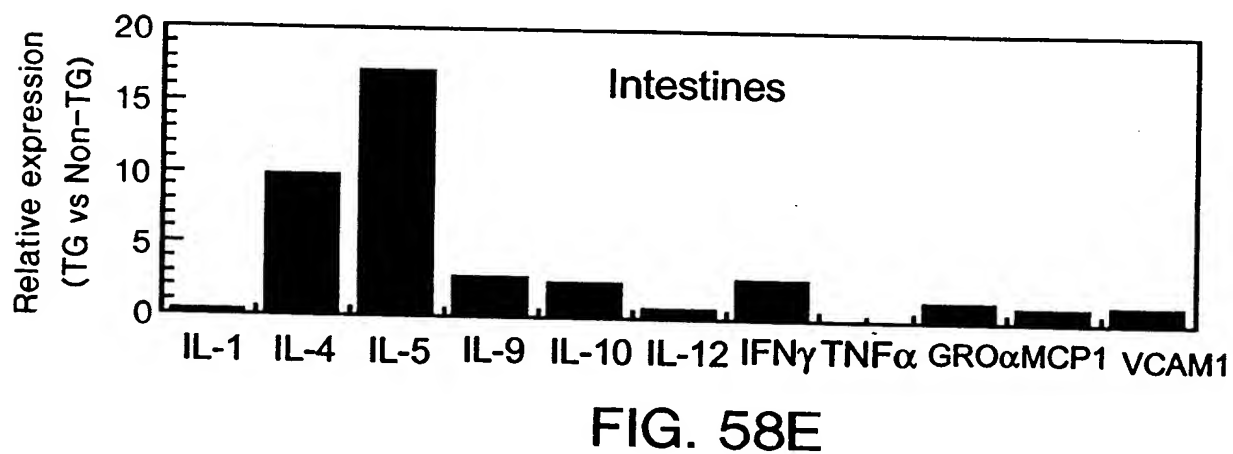
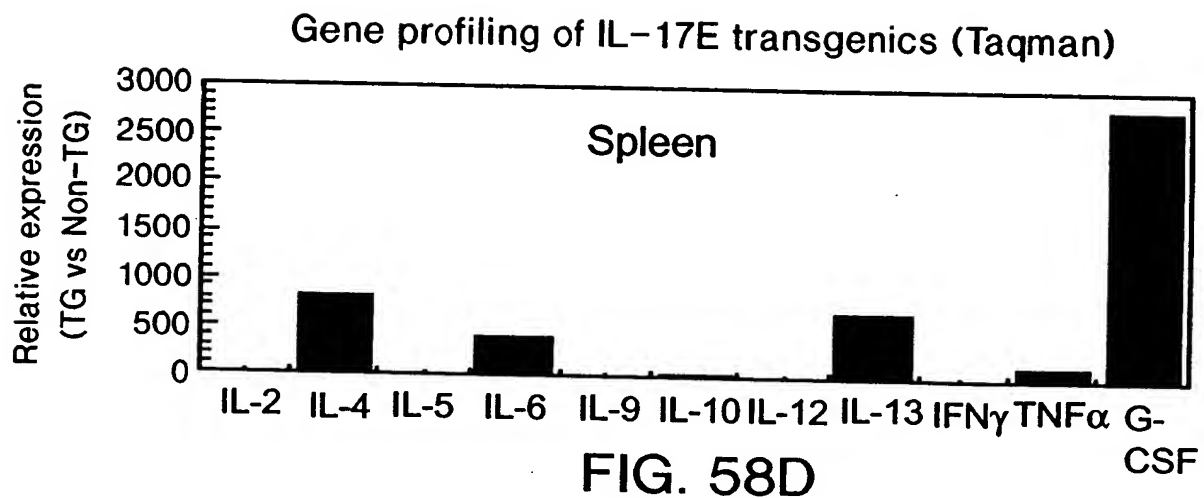


FIG. 58C



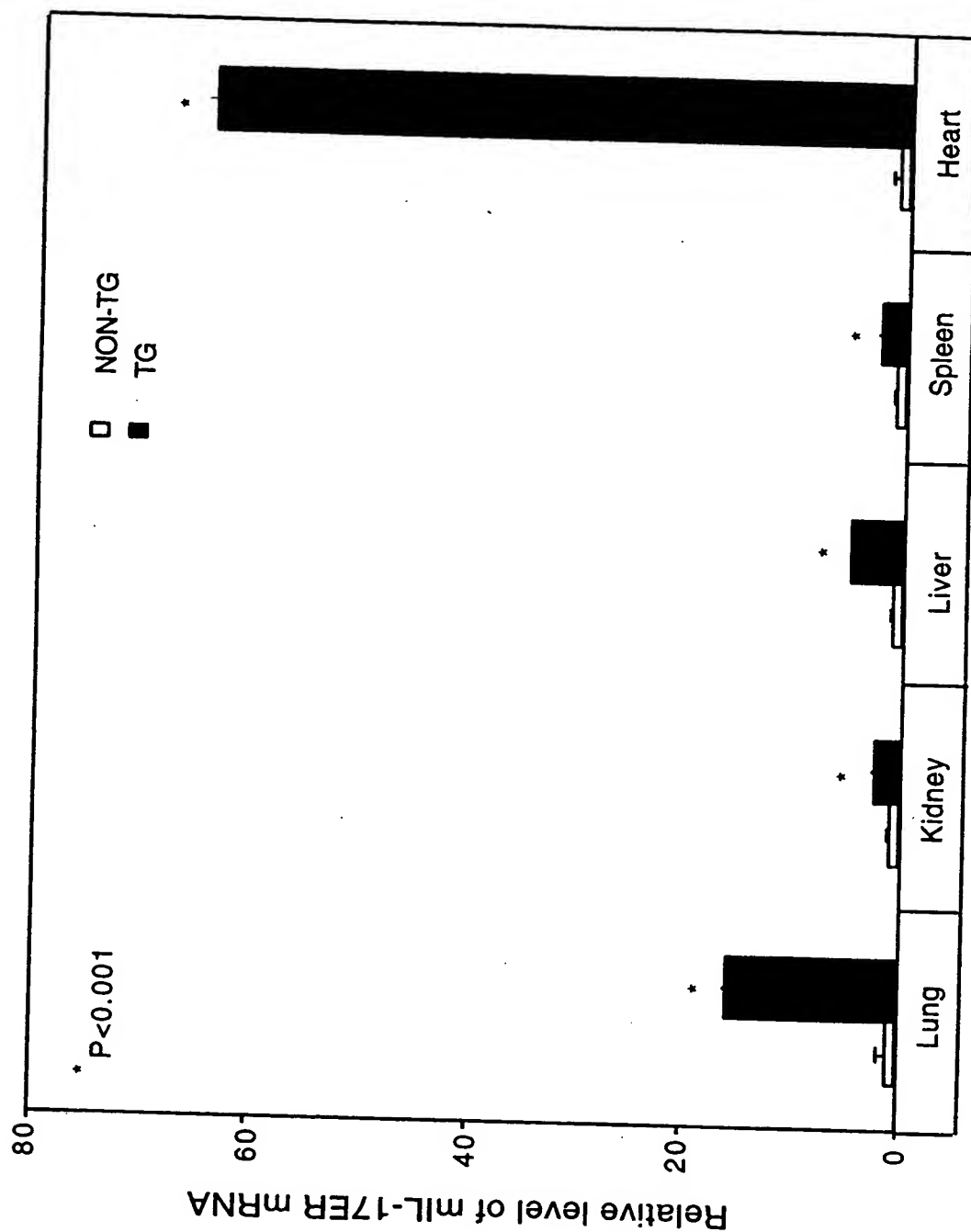


FIG. 59

Elevated serum IL-5, IL-13 and TNF α
in mIL-17E transgenics

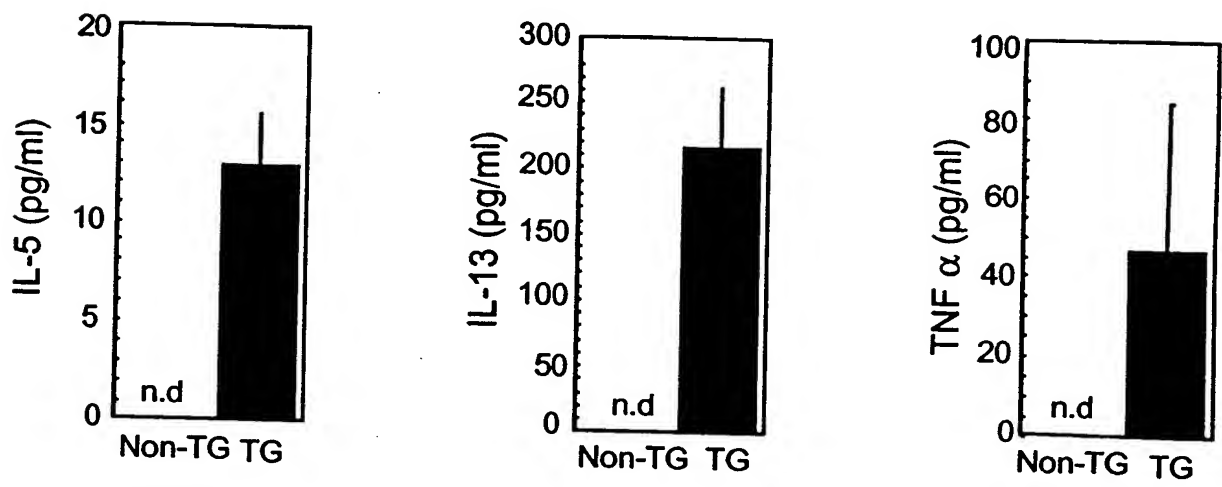


FIG. 60

Serum IgE and IgG1, but not IgG2a is elevated
in mL-17E transgenics

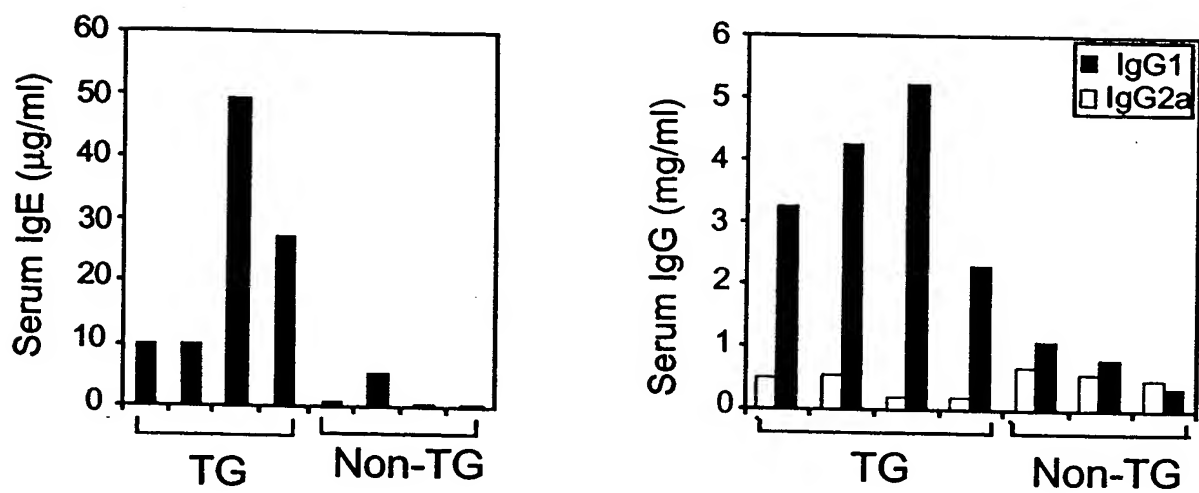


FIG. 61

Neutrophilia in mIL-17E transgenics
(8 wks, PBMC by FACS)

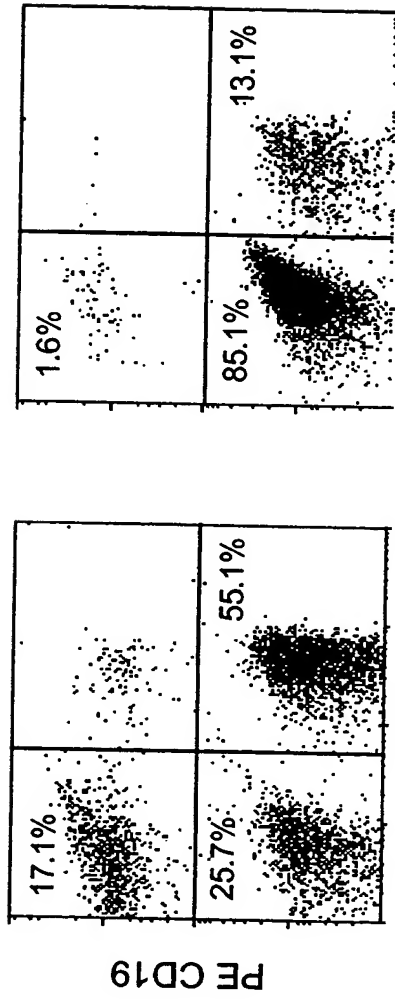


FIG. 62A

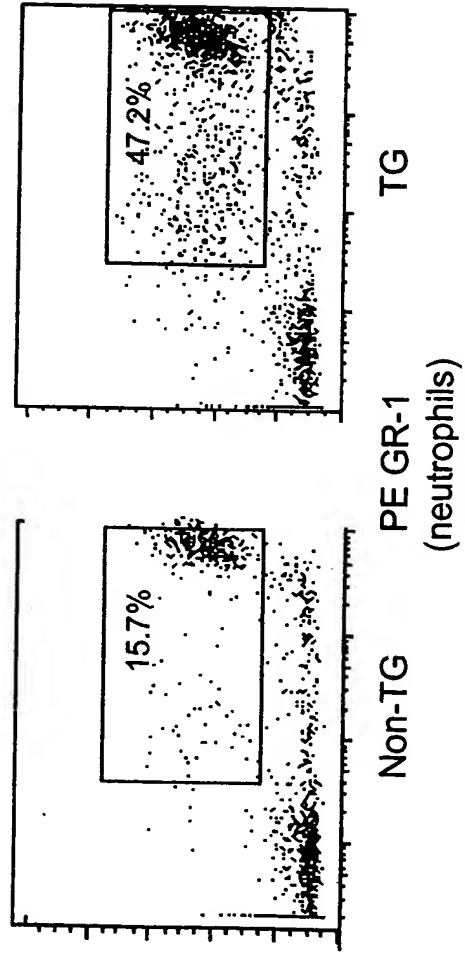


FIG. 62B

Neutrophilia and eosinophilia in mIL-17E transgenics (hematology)

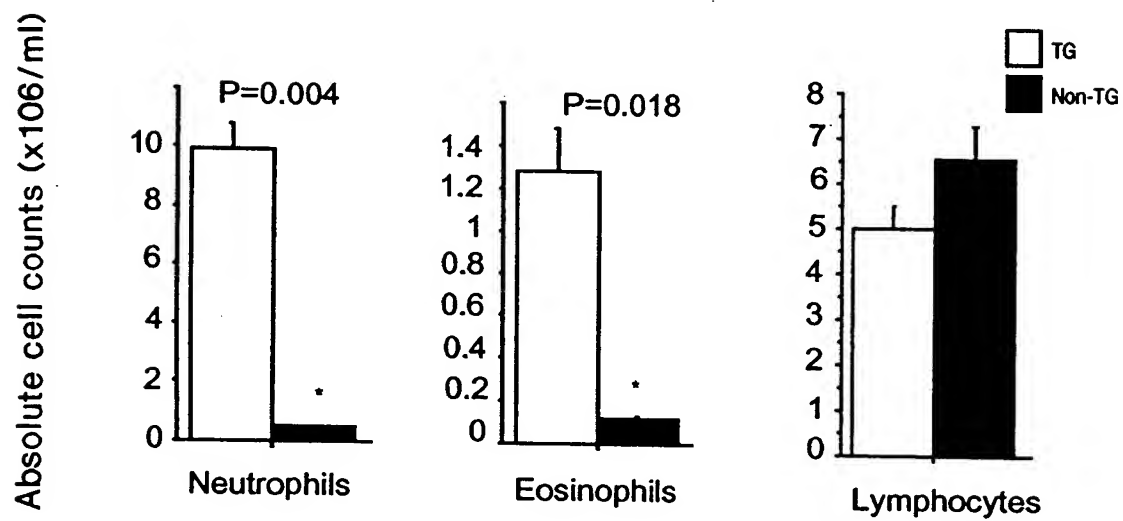


FIG. 63

G-CSF is elevated in
mIL-17E transgenics

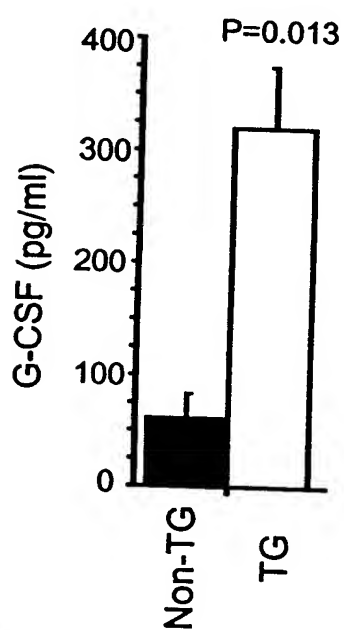
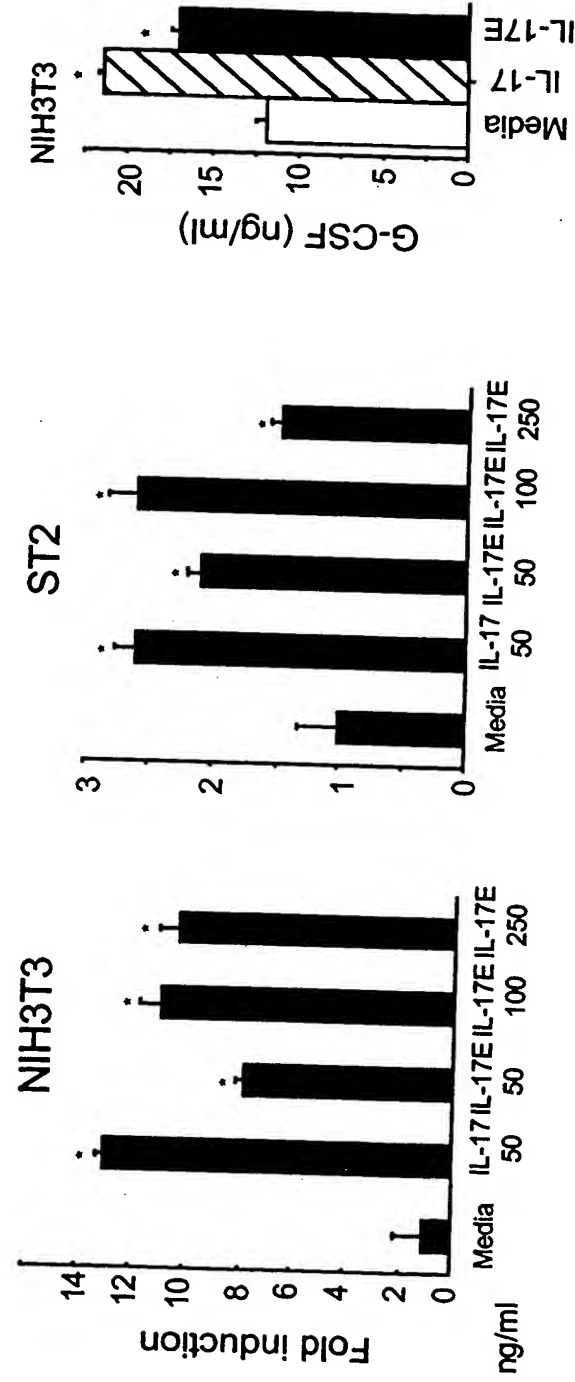


FIG. 64

IL-17E induces production of G-CSF in vitro



*P<0.05

FIG. 65

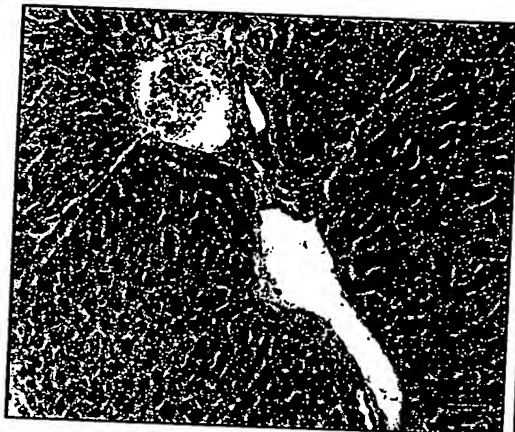


FIG. 66A

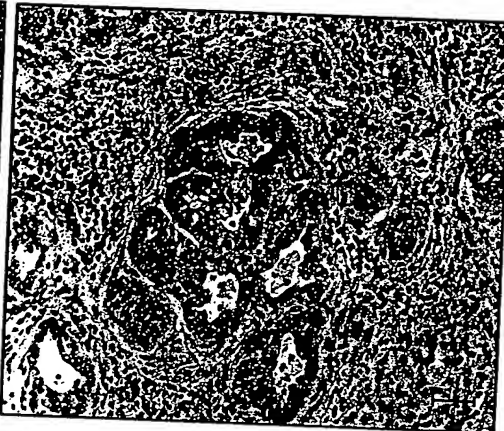


FIG. 66B



FIG. 66C

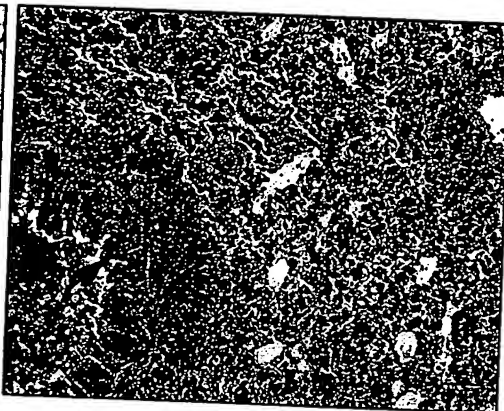


FIG. 66D